



# **STIC Search Report**

## **Biotech-Chem Library**

### **STIC Database Tracking Number:**

**TO: Terra Gibbs**  
**Location: CM1/12A12/11E12**  
**Art Unit: 1635**  
**Thursday, June 19, 2003**

**Case Serial Number: 998667**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**CM1-6A06**  
**Phone: 605-1155**

**maryjane.ruhl@uspto.gov**

### **Search Notes**



**From:** Gibbs, Terra  
**Sent:** Wednesday, June 18, 2003 12:45 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search request...

96916

Could you please do a regular search of SEQ ID NO: 1 of USSN 09/998667?

Thank You!

**Terra Gibbs**  
**AU 1635**  
**306-3221**  
**Mailbox: 11E12**

CFE

Mary Jane Ruhl  
Tech. Info. Specialist, STIC  
TC-1600  
CM-1, Room 6A-06  
Phone: 605-1155









PT such as central nervous system injuries.

PS Example 2: SEQ ID NO 6745; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA438642-AA439233) with neurotrophic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis and Shy-Drager Syndrome. Other uses include the  
 CC utilization of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the prior art  
 CC specification.

XX Sequence 196 AA:

Query Match 58.4%; Score 734, DB 22; Length 196;  
 Best Local Similarity 100.0%; Pred No. 4 1e-70;  
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSVLTDSCKSAPASATATALERRRDEPLPTSPFCACVLEVLHQPETRCGHVPCSC 60  
 DB 61 MGSVLTDSCKSAPASATATALERRRDEPLPTSPFCACVLEVLHQPETRCGHVPCSC 120  
 QY 61 IATSKNNKKTCTPCYCAVLPSEGVPAIDVAKRKSEYKNCACDILVLSMRHITTCQ 120  
 DB 121 IATSKNNKKTCTPCYCAVLPSEGVPAIDVAKRKSEYKNCACDILVLSMRHITTCQ 180  
 QY 121 KYIDKYGFLPLEETA 136  
 DB 181 KYIDKYGFLPLEETA 196

RESULT 5  
 AAB97205  
 ID AAB97205 standard; Protein: 228 AA.

XX AAB97205;

XX 28-JUN-2002 (first entry)

XX Novel human protein SEQ ID NO: 473.

XX Human: antihaemetic; vulnerrary; antinflammatory; immunomodulator;  
 KW antifertility; cerebroprotective; cytostatic; therapeutic; gene therapy;  
 KW neuroprotective; antiParkinsonian; protein therapy; EST;  
 KW expressed sequence tag.

XX Homo sapiens.

XX W0206222649-A2.

XX 21-MAR-2002.

XX 10-SEP-2001, 2001WO 0326015.

XX 11-SEP-2000; 2000US-0659671.

XX (HYSE-) HYSEQ INC.

XX Tanq YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao GA, Ren F;

XX Xue AJ, Yang Y, Wehrman T, Dmanac RT;

XX WP1: 2002-292408/33.

XX N-PSDB: ABN12341.

PT An isolated polynucleotide for treating diseases associated with its  
 CC encoded polypeptide such as cancer and multiple sclerosis

PS Example 2: SEQ ID NO 473; 509pp; English.

XX The present invention provides the protein and coding sequences of 444  
 CC novel human proteins. These were isolated from expressed sequences tags  
 CC (ESTs). They can be used to stimulate cell growth, to regulate  
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue growth  
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
 CC Parkinson's disease. The present sequence is a protein of the invention.

XX Sequence 228 AA:

Query Match 27.8%; Score 349, DB 23; Length 228;  
 Best Local Similarity 31.3%; Pred No 6 7e-29;  
 Matches 72; Conservative 51; Mismatches 85; Indels 22; Gaps 6;

QY 8 DSGKSAPASATATALERRRDEPLPTSPFCACVLEVLHQPETRCGHVPCSC 67  
 DB 7 DSGKSAPASATATALERRRDEPLPTSPFCACVLEVLHQPETRCGHVPCSC 126  
 QY 68 NKWTCYCAVLPSEGVPAIDVAKRKSEYKNCACDILVLSMRHITTCQ 126  
 DB 60 NKWTCYCAVLPSEGVPAIDVAKRKSEYKNCACDILVLSMRHITTCQ 117  
 QY 127 -GHVLEETAR-----CVCPCG-RELYEYSLDHCITTHSRERPRVPC 174  
 DB 118 MEGKATIKASLQPPNNVNNKTPCYCPCKNNQGEIVHCKLEPSTDKSVCP 177  
 QY 175 LIPENSSPSGNIIRHLOVSHITLYDPIDPNIIRVALIRVLDKSLAE 224  
 DB 178 SMPGCDPNYSANREHILQRRHPSYITVDIVDEFLMNOVIGRSIID 227

RESULT 6  
 AAB43861  
 ID AAB43861 standard; Protein: 231 AA.

XX AAB43861;

XX 08-FEB-2001 (first entry)

XX Human cancer associated protein sequence SEQ ID NO:1306.

XX Human: cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnerrary; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; anti;  
 KW antiinflammatory; antitumor; antiallergic; antibacterial; cardiac;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nucleotypic;  
 KW vasotropic; antiproliferative; antiaquogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.

XX Homo sapiens.

XX W0200053550-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-0505882.

XX 12 MAR 1999; 9903-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;





[illegible]

FA	(HUMA ) HUMAN GENOME SCI INC.
XX	
F1	Koscius CA, Barash SC, Ruben SM;
XX	WPI: 2001-448783/53.
D8	R FSDBY: AAS26326.
HE	
XX	New nucleic acid molecules encoding 461 human secreted proteins for
PT	diagnosing, preventing, treating or ameliorating medical conditions and
PT	used as food additives or preservatives -
XX	Citation 11, SPQ ID No.1992, 980pp; English.
XX	
CC	The invention relates to isolated nucleic acid molecules and their
CC	encoded secreted proteins. The nucleic acids and proteins are used to
CC	prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC	rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC	are also used in diagnosing a pathological condition or susceptibility
CC	to a pathological condition. Antibodies to the proteins can also
CC	be used in alleviating symptoms associated with the disorders and in
CC	diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC	immunosorbent assays (ELISA) disorders which are diagnosed or treated
CC	include autoimmune diseases e.g. rheumatoid arthritis,
CC	hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC	cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC	e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC	Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC	and other disorders e.g. corneal infection, and many other
CC	disorders listed in the specification. The polypeptides can also
CC	be used to aid wound healing and epithelial cell proliferation, to
CC	prevent skin aging due to sunburn, to maintain organs before
CC	transplantation, for supporting cell culture of primary tissues, to
CC	regenerate tissues and in chemotaxis. The polypeptides can also be used
CC	as a food additive or preservative to increase or decrease storage
CC	capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC	minerals, cofactors and other nutritional components. The present
CC	sequence represents a novel secreted protein of the invention.
CC	
Query Match	27.8%, Score 349, DB 22, Length 231:
Best local Similarity	31.3%, Pred. No. 6,80-29;
Matches	72, Conservative 51, Mismatches 95, Indels 22, Gaps 6
E7	8 PSEKSNASTAVALLPFRPPRLPTSPYVGLFHLHGVVFPGSVPRGATLNLN 67
EE	19 DGGAGQLAGRAEAD RERTTIVCLVTRKYLVNGHVPSACLLDLETLT 62
E9	68 NKRTFYCYRAYLSDECVATVAERKCEYRCADELTVLSEMAHPLRYGYLDKY 126
E6	63 KRVGVCGESALAPGVAAVLELPDLFSLISQCKRNKRPELKKIKSHVATSKY GRV 120
E7	127 GTIDELLETPAR ... CVCGRD QGNATKSHLLPRTTHIRSRKRRVPPDR 174
E4	121 MEQVATTEAELGCPHNINVEYTFPGVGPENITGNNVMDIKLDTHTKRSVPICA 180
E7	175 LFDENSSFSCHLLEHLVAETLELYNEIDNILEPALIPVYLWDLE 224
E4	181 SMWLTNYRKANFEHIEFHIFRSYTFVAYVMILMRGVLAGSIP 230
RESULT 8	
AAG75629	
ID	AAG75629 standard; Protein; 231 AA.
XX	
AC	AAG75629;
XX	
F1	03 SEP 2001 (first entry)
XX	
DE	Human colon cancer antigen protein SPQ ID No:6393.
XX	
EM	Human, colon cancer; colon cancer antigen; diagnosis; detection;
EM	colorectal carcinoma.
OS	Homo sapiens.







[illegible]

16	17 NOV 2000	2360035-0249245	16	17 NOV 2000	2360035-0249245
17	17 NOV 2000	2360035-0249264	17	17 NOV 2000	2360035-0249264
18	17 NOV 2000	2360035-0249265	18	17 NOV 2000	2360035-0249265
19	17 NOV 2000	2360035-0249297	19	17 NOV 2000	2360035-0249297
20	17 NOV 2000	2360035-0249400	20	17 NOV 2000	2360035-0249400
21	01 DEC 2000	2360035-0250160	21	01 DEC 2000	2360035-0250160
22	01 DEC 2000	2360035-0250491	22	01 DEC 2000	2360035-0250491
23	05 DEC 2000	2360035-0251030	23	05 DEC 2000	2360035-0251030
24	05 DEC 2000	2360035-0251488	24	05 DEC 2000	2360035-0251488
25	05 DEC 2000	2360035-0256719	25	05 DEC 2000	2360035-0256719
26	09 DEC 2000	2360035-0251856	26	09 DEC 2000	2360035-0251856
27	09 DEC 2000	2360035-0251868	27	09 DEC 2000	2360035-0251868
28	09 DEC 2000	2360035-0251869	28	09 DEC 2000	2360035-0251869
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30	11 DEC 2000	2360035-0251990	30	11 DEC 2000	2360035-0251990
31	05 JAN 2001	2360035-0254937	31	05 JAN 2001	2360035-0254937
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07-JUN-2000: 2000IS-0209467

PR 28-JUN-2000; 2000MS-0214886

[illegible]









DB 16 FVAVGVAVLALPVLAHGVHVPVCHLLAMRSLHCHLHGSVLPREFACVFAALL 75  
QY 87 TVAKRMSEVYKALPTLVLSMAHETQKYIDKQ ---FGELEPTAAK 179  
DB 76 FNMKRFSG---SCLVSKLKHYPMPHYVSTVYQVYGVSVLHNFKLQSVSSN 142  
QY 140 -----VCPGORELY-EDSLDHCITTHRSRRHVPQPIQ 173  
DB 133 RSELSASNTETLYQELTSSSHPTKPKPLCOESNTRKRLDHCNSNHLQIVVTCPTC 192  
QY 174 KLPENPSPSGNLPRLGVSHTLFVDFINFTLFPALLPVLDES 221  
DB 193 VSLPMDPSQITLNFVSH NCPHGVYGEFVNLQDEFTQVQVAES 240

RESULT 2  
US-09-252-429-36  
Sequence 36, Application US/09252329  
Patent No. 6147192  
GENERAL INFORMATION:  
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
TITLE OF INVENTION: Theoret  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & CORFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/252,429  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/497,340  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silveri, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-005CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-252-329-46

Query Match 23.5% Score 295; DB 4; Length 245;  
Best local Similarity 28.5% Pred. No. 1,9e+25;  
Matches 65; Conservative 45; Mismatches 84; Indels 44; Gaps 6;

QY 45 FVCAVAVLHGVAVP-TPGVHVPVSCVATISLKNKKKMGVGVAVLP-----SRGVFA 86  
DB 16 FVGVGVAVLKTVPKAAQVHVPKRCVLTAMPESGTHQPIVGVSVLPBPVCPVPAPI 75  
QY 87 TVAKRMSEVYKALPTLVLSMAHETQKYIDKQ ---FGELEPTAAK 179  
DB 76 FNMKRFSG---SCLVSKLKHYPMPHYVSTVYQVYGVSVLHNFKLQSVSSN 142  
QY 140 -----VCPGORELY-EDSLDHCITTHRSRRHVPQPIQ 173

DB 133 RSELSASNTETLYQELTSSSHPTKPKPLCOESNTRKRLDHCNSNHLQIVVTCPTC 192  
QY 174 KLPENPSPSGNLPRLGVSHTLFVDFINFTLFPALLPVLDES 221  
DB 193 VSLPMDPSQITLNFVSH NCPHGVYGEFVNLQDEFTQVQVAES 240

RESULT 3  
US-08-897-340-35  
Sequence 35, Application US/08897340  
Patent No. 5955306  
GENERAL INFORMATION:  
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
TITLE OF INVENTION: Theoret  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & CORFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,340  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/715,032  
FILING DATE: 17-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Silveri, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-005CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-897-340-35

Query Match 22.5% Score 283; DB 2; Length 245;  
Best local Similarity 30.7% Pred. No. 4.3e+24;  
Matches 66; Conservative 28; Mismatches 83; Indels 38; Gaps 6;

QY 35 FVCAVAVLHGVAVP-TPGVHVPVSCVATISLKNKKKMGVGVAVLP-----SRGVFA 89  
DB 16 FVGVGVAVLKTVPKAAQVHVPKRCVLTAMPESGTHQPIVGVSVLPBPVCPVPAPI 75  
QY 87 TVAKRMSEVYKALPTLVLSMAHETQKYIDKQ ---FGELEPTAAK 176  
DB 76 FNMKRFSG---SCLVSKLKHYPMPHYVSTVYQVYGVSVLHNFKLQSVSSN 145  
QY 140 -----VCPGORELY-EDSLDHCITTHRSRRHVPQPIQ 173

RESULT 4

[illegible]

TYPE: amino acid  
TOPOLGY: linear  
MOLECULE TYPE: protein  
MS: 08-639-237-2

Query Match	12.38;	Score 155;	DB 1;	Length 522;
Best Local Similarity	24.28;	Prod. No. 4.1e-09,		
Matches 54;	Conservative 24;	Mismatches 69;	Indels 76;	Gaps 8;

07	2	DEPRLVTSI:SGCAGTCEVLQVAVTICGNGHVSCTATSIKKNKWTGCPRAVPIPSFCVRA	86
07	1	1 1	
0b	61	DPRLPE-SKVCSPICGLMABRAVQVPGNGHVSQACI1KSI1PDAQKSPVDNFI1LENDQ1P	119
07	87	TIVAKREKSTYKMACTIIVL1SEMKAIK1QVATUKVSGDLETAARCV-----C	141
07	1	1 1	
0b	120	DNEAKR--ELLSLMVKCPGNSCKHKE-----LKLDELHQAHCERALMDK	162
07	142	PRQVREYELSLDNGTTHNRSPRRVPRGSC--R1LTPEN-----	180
07	1	1 1	
0b	163	PCVQVPRQKNGT1HILKQ--GVPRQVSTKQDASMAFRDKEIPIQNGT1AAVLSTVNT	220
07	181	-----PSFSF-----GNELPHQ	193
07	1	1 1	
0b	221	1111REGQVNIHYDLSCEIAP1PCL1SI1GSCNKKMK1N1LAKH1Q	263

RESULT 7  
US-08-975-405-2  
; Sequence 2, Application US/08975405

1 GENERAL INFORMATION:  
2 APPLICANT: Goeddel, David V.  
3 APPLICANT: Xiong, Jesse  
4 TITLE OF INVENTION: No. 5767244e1 Protein - TRAF6  
5 NUMBER OF SEQUENCES: 2  
6 CORRESPONDENCE ADDRESS:  
7 ADDRESSEE: Fleury, Holbach, Test, Albritton & Herbert  
8 STREET: 4 Embarcadero Center, Suite 3400  
9 CITY: San Francisco  
10 STATE: California  
11 COUNTRY: USA  
12 ZIP: 94111  
13 COMPUTER READABLE FORM:  
14 MEDIUM TYPE: floppy disk  
15 COMPUTER: IBM PC compatible  
16 OPERATING SYSTEM: PC-DOS/MS-DOS  
17 SOFTWARE: Patcon in Release #1.0, Version #1.30  
18 CURRENT APPLICATION DATA:  
19 APPLICATION NUMBER: US/09/975,405  
20 FILING DATE:

Query Match: 12.38; Score 155, DB 1, Length 522,  
Best Local Similarity 24.28; Pred. NO 4 1e-09;  
Matches 54; Conservative 24; Mismatches 69; Indels 76, Gaps 8

[illegible]

RESULT 8  
US-09-138-277C-1  
Sequence 1, Application US/09138277C

```

1  GENERAL INFORMATION:
2  APPLICANT: NAKATA, MOTOMI
3  APPLICANT: NAKANO, HIROYASU
4  APPLICANT: YAGITA, HIDEO
5  APPLICANT: OKUMURA, KO
6  TITLE OF INVENTION: TRAP FAMILY MOLECULES, POLYNUCLEOTIDES ENCODING THEM
7  TITLE OF INVENTION: AND ANTIBODIES AGAINST THEM
8  FILE REFERENCE: 007848-025515
9  CURRENT APPLICATION NUMBER: US/09/138,277C
10 CURRENT FILING DATE: 1998-08-18
11 PRIOR APPLICATION NUMBER: PCT/JP97/00512
12 PRIOR FILING DATE: 1997-02-24
13 PRIOR APPLICATION NUMBER: JP 44674/1996
14 PRIOR FILING DATE: 1996-02-22
15 NAME OF SEQ ID NO:8: 16
16 SOFTWARE: PatentIn Ver. 2.1
17 SEQ ID NO 1
18 LENGTH: 558
19 TYPE: PRT
20 ORGANISM: Mus sp.
21 US-09-138-277C-1

```

	Query Match	11.8%	Score 148.5	DH 4	Length 548;
	Best Local Similarity	25.0%	Eved No. 2,560-46		
	Matches	411	Conservative	27	Mismatches 59; Indels 37; Gaps 6.
QY	35	PDEAWLEVDVHCVRGCRKSLATSKNNRWLCFQAKALSHGVALLNARK	92		
		: : : : :   : : : : :   : : : : :   : : : : :			
DB	43	YKAPRHSVNLHNDRGCHPFGDGLPSLPRLNSVPDTGVKEVKIQLGVDFKDNCKRK	101		
		: : : : :   : : : : :   : : : : :   : : : : :			
QY	93	MRESEYNASTTDLVLTSEMKVALPTG-----GGFTLVYS	127		
		: : : : :   : : : : :   : : : : :   : : : : :			
DB	102	EVLNLIVYCSKNAGSMAKLTLRRFDNDYDSFGADVCPNRSKRAMLRKYKKELISAYC	161		
		: : : : :   : : : : :   : : : : :   : : : : :			
QY	128	PLDLETETARCVPRCPRELPEYSLDILCTTHNRSPRYLPTCL	171		
		: : : : :   : : : : :   : : : : :   : : : : :			
DB	142	PPRPFRK-----LYVGRVAVLNIGWQHTFNSTPAVVVSPL	196		
		: : : : :   : : : : :   : : : : :   : : : : :			

```

1  RESULT: 9
2  US-09-268-544R-36
3  ? Sequence 36, Application US/09268544R
4  ? Patent No. 6410710
5  ? GENERAL INFORMATION:
6  ? APPLICANT: Ledgerman, Seth
7  ? APPLICANT: van Bynhoven, Wilfried
8  ? TITLE OF INVENTION: TRA-3 deletion isoforms And Uses Thereof
9  ? FILE REFERENCE: 0575-58732
10 ? CURRENT AFFILIATION NUMBER: 2873/268-544R
11 ? CURRENT FILING DATE: 1999-03-11
12 ? NUMBER OF SEQ ID NOS: 43
13 ? SOFTWARE: PatentIn Ver. 2.1

```



```

1  FILING DATE: 14-MAR-1997
2  ATTORNEY/AGENT INFORMATION:
3  NAME: Campbell, Cathryn A.
4  REGISTRATION NUMBER: 31,015
5  REFERENCE/DOCKET NUMBER: P-1-J 3209
6  TELECOMMUNICATION INFORMATION:
7  TELEPHONE: (619) 535-0001
8  TELEFAX: (619) 535-8949
9  INFORMATION FOR SEQ ID NO: 6:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 450 amino acids
12 TYPE: amino acid
13 TOPOLOGY: Linear
14 US-09-115-934A-6
15
16 Query Match 10-38; Score 130; DB 4; Length 450;
17 Best Local Similarity 32-28; Pct. Id. 73.33%;
18 Matches 29; Conservative 12; Mismatches 37; Gaps 10; Gaps 3
19
20
21 14 PANSATAPALEPFD-----PELPVTSPPAVCLEVLEHLPVLPVPPGVHVGPGSLATSR 66
22 1 : : : 11 : : : 1 : 1 : : 1 : 11 11 1 : :
23 4 POKSYVNTMLDEPDEKSTGGQSVSEPSCHYYDILVNDITLTMVGHSPKRLALMAA 63
24
25 67 NNRKWT-CPPYRATVPSFVYATDAKK 92
26 : : 1 1 1 11 : 1 1 : 1
27 64 SSKKTECPKTR-KKKGPPKVSILIK 88
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29
30 RESULT 14
31 US-09-230-196-5
32 Sequence 5; Application US/09240196
33 Patent No. 6307035
34
35 GENERAL INFORMATION:
36 APPLICANT: Rauscher III, Frank J.
37 APPLICANT: Jensen, David E.
38 TITLE OF INVENTION: HPCAI Associated Protein (BAP-1) and
39 TITLE OF INVENTION: Uses Thereof
40 NMRPP OF SEQUENCES: 47
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Howson and Howson
43 STREET: Spring House Corporate Cntr., P.O. Box 457
44 CITY: Spring House
45 STATE: Pennsylvania
46 COUNTRY: U.S.A.
47 ZIP: 19477
48
49 COMPUTER READABLE FORM:
50 MEDIUM TYPE: Floppy disk
51 COMPUTER: IBM pc compatible
52 OPERATING SYSTEM: PC DOS/MS-DOS
53 SOFTWARE: Patent Release #1.0, Version #1.30
54 CURRENT APPLICATION DATA:
55 APPLICATION NUMBER: US/09/240,196
56 FILING DATE:
57
58 CLASSIFICATION:
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: US 60/022,997
61 FILING DATE: 02-AUG-1996
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: US 60/048,109
64 FILING DATE: 19-FEB-1997
65
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Bak, Mary E.
68 REGISTRATION NUMBER: 31,215
69 REFERENCE/DOCKET NUMBER: WSI68BUSA
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: 215-540-9200
72 TELEFAX: 215-540-5818
73 INFORMATION FOR SEQ ID NO: 5:
74 SEQUENCE CHARACTERISTICS:
75 LENGTH: 100 amino acids
76 TYPE: amino acid
77 STRANDEDNESS:
78 TOPOLOGY: unknown
79

```





100

100



QY 181 PSSPSCNLIKRLQVSHI...FYDGF...LPPV...LHSL...LEVYHNSRT 232  
 DB 181 PSSPSCNLIKRLQVSHI...FYDGF...LPPV...LHSL...LEVYHNSRT 232

## RESULT 2

US-09-998-667-7  
 ? Sequence 7: Application US/09998667  
 ? Patent No. US20020146747A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Masuda, Esteban  
 ? APPLICANT: Liao, X. Charlene  
 ? APPLICANT: Zhao, Baoxian  
 ? APPLICANT: Chu, Peter  
 ? APPLICANT: Pardo, Jorge  
 ? APPLICANT: Rigel Pharmaceuticals, Incorporated  
 ? TITLE OF INVENTION: TRAC1: Modulators of Lymphocyte Activation  
 ? FILE REFERENCE: 021044-000600DS  
 ? CURRENT APPLICATION NUMBER: US/09/998,667  
 ? CURRENT FILING DATE: 2001-12-03  
 ? PRIOR APPLICATION NUMBER: US 60/282,432  
 ? PRIOR FILING DATE: 2001-04-06  
 ? NUMBER OF SEQ ID NOS: 18  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 7  
 ? LENGTH: 239  
 ? TYPE: PRT  
 ? ORGANISM: Mus sp.  
 ? FEATURE:  
 ? OTHER INFORMATION: mouse TRAC1 protein (3rd frame)  
 ? NAME/KEY: M1\_FFS  
 ? LOCATION: (3)  
 ? OTHER INFORMATION: Xaa = Arg or Ser  
 ? FEATURE:  
 ? NAME/KEY: M1\_PES  
 ? LOCATION: (4)  
 ? OTHER INFORMATION: Xaa = Met, Val or Leu  
 ? OTHER INFORMATION: Xaa = Met, Val or Leu  
 ? US-09-998-667-7

## Query Match

Best Local Similarity 86.2%; Score 1083.5; DB 10; Length 239;  
 Matches 198; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 GSVLSTDSKSPASAPATAAPALFPPDPPELVPTSPVAVCI FVILHQPVPPTPGHVECPSC1 61  
 DB 5 GSVLSTDSKSPASAPATAAPALFPPDPPELVPTSPVAVCI FVILHQPVPPTPGHVECPSC1 64  
 QY 62 AISKNNKWKTCPCYCAVIFSEGVAVDIDAFPMSTYQNAFCCTIVLITMPAHITPTC 124  
 DB 65 AISKNNKWKTCPCYCAVIFSEGVAVDIDAFPMSTYQNAFCCTIVLITMPAHITPTC 124  
 QY 121 KYIDKYGPIOLEEFTAAFCVCPFGVCPVYFVLSLHRCITTHRSRPPVPCITCLIFCN 180  
 DB 125 KYIDKYGPIOLEEFTAAFCVCPFGVCPVYFVLSLHRCITTHRSRPPVPCITCLIFCN 184  
 QY 181 PSSPSCNLIKRLQVSHI...FYDGF...LPPV...LHSL...LEVYHNSRT 232  
 DB 185 PSSPSCNLIKRLQVSHI...FYDGF...LPPV...LHSL...LEVYHNSRT 236

## RESULT 3

US-09-949-842-19  
 ? Sequence 19: Application US/09949842  
 ? Patent No. US2002016462A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Ni et al.  
 ? TITLE OF INVENTION: PT047P1  
 ? FILE REFERENCE: Immune System-related Polynucleotides, Polypeptides, and Antibodies  
 ? CURRENT APPLICATION NUMBER: US/09/949,842  
 ? CURRENT FILING DATE: 2001-09-02  
 ? PRIOR APPLICATION NUMBER: PCT/US01/07370

? PRIOR FILING DATE: 2001-03-07  
 ? PRIOR APPLICATION NUMBER: 69/224,367  
 ? PRIOR FILING DATE: 2000-08-11  
 ? PRIOR APPLICATION NUMBER: 60/187,873  
 ? PRIOR FILING DATE: 2000-03-08  
 ? NUMBER OF SEQ ID NOS: 26  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 19  
 ? LENGTH: 185  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 ? US-09-949-842-19

## Query Match

Best Local Similarity 73.1%; Score 919; DB 9; Length 185;  
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSVLTDSKSPASAPATAAPALFPPDPPELVPTSPVAVCI FVILHQPVPPTPGHVECPSC1 60  
 DB 1 MGSVLTDSKSPASAPATAAPALFPPDPPELVPTSPVAVCI FVILHQPVPPTPGHVECPSC1 60  
 QY 61 IATSLKNNKWKTCPCYCAVIFSEGVAVDIDAFPMSTYQNAFCCTIVLITMPAHITPTC 120  
 DB 61 IATSLKNNKWKTCPCYCAVIFSEGVAVDIDAFPMSTYQNAFCCTIVLITMPAHITPTC 120  
 QY 121 KYIDKYGPIOLEEFTAAFCVCPFGVCPVYFVLSLHRCITTHRSRPPV 168  
 DB 121 KYIDKYGPIOLEEFTAAFCVCPFGVCPVYFVLSLHRCITTHRSRPPV 168

## RESULT 4

US-10-205-823-455  
 ? Sequence 455: Application US/10205823  
 ? Publication No. US20030108963A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Schlegel, Robert  
 ? APPLICANT: Monahan, John E.  
 ? APPLICANT: Fudenberg, John O.  
 ? APPLICANT: Gannavarapu, Manjula  
 ? APPLICANT: Gorbacheva, Bella  
 ? APPLICANT: Hoersch, Sebastian  
 ? APPLICANT: Kamatkar, Shubhangi  
 ? APPLICANT: Womsey, Angela M  
 ? APPLICANT: Clact, Karen  
 ? APPLICANT: Zhaio, Xumei  
 ? APPLICANT: Anderson, Dustin  
 ? TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ? TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ? FILE REFERENCE: MK1-044  
 ? CURRENT APPLICATION NUMBER: US/10/205,823  
 ? CURRENT FILING DATE: 2002-07-25  
 ? PRIOR APPLICATION NUMBER: 60/407,982  
 ? PRIOR FILING DATE: 2001-07-25  
 ? PRIOR APPLICATION NUMBER: 60/414,356  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR APPLICATION NUMBER: 60/425,020  
 ? PRIOR FILING DATE: 2001-09-25  
 ? PRIOR APPLICATION NUMBER: 60/441,746  
 ? PRIOR FILING DATE: 2001-12-12  
 ? PRIOR APPLICATION NUMBER: 60/362,158  
 ? PRIOR FILING DATE: 2002-04-05  
 ? NUMBER OF SEQ ID NOS: 455  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO 455  
 ? LENGTH: 228  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 ? US-10-205-823-455

## Query Match

Best Local Similarity 31.8%; Score 149; DB 9; Length 228;  
 Matches 73; Conservative 11; Mismatches 95; Indels 22; Gaps 6;



Db 121 MEGVAKATIKDASLOPBNVNPRTFPYFPEKPNQDEGLVECKPLPHSTDTKRSVCPICA 180  
 QY 175 LIPDENPSSFCNLIIRHIOVSHTLEYPDLOPNIIEPALIRVLDORSLIE 224  
 Db 181 SMWGDIPNRSANPFRHIGRPHRESYDIFVDVDEDMNMCVLQESILD 230

## RESULT 8

US-09-764-864-1292  
 ? Sequence 1292, Application US/09764864  
 ? Patent No. US20020132753A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Rosen et al.  
 ? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ? FILE REFERENCE: PT223  
 ? CURRENT APPLICATION NUMBER: US/09/764,864  
 ? CURRENT FILING DATE: 2001-01-17  
 ? Prior application data removed - consult PALM or file wrapper  
 ? NUMBER OF SEQ ID NOS: 1792  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 1292  
 ? LENGTH: 231  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-09-764-864-1292

Query Match 27.8%; Score 340; DB 10; Length 231;  
 Host Local Similarity 31.3%; Pred. No. 3, 7e-25;  
 Matches 72; Conservative 0; Mismatches 85; Indels 22; Gaps 0.

QY 8 DSKSAPASATAPALPPRPDPPELVTSFPCVACLEVLHQVPVTCGVHPCRSYIATSLKN 67  
 Db 10 DSKSAPASATAPALPPRPDPPELVTSFPCVACLEVLHQVPVTCGVHPCRSYIATSLKN 62  
 QY 68 NKMTGPGYCAVLEHGVAVTAVAKPKSKYKAWAPPTVTSIMRAHIFGQYLUKY 125  
 Db 63 KRIYGVCPSSALAPGVPAVLEFPGESTETSCHEGPKNFELSKLASHVATQSY 120  
 QY 127 --GPDLELEETAR-----GVPPG--GPELYEYSLDHCITHHSEPPVPCVLCR 174  
 Db 121 MEGVAKATIKDASLOPBNVNPRTFPYFPEKPNQDEGLVECKPLPHSTDTKRSVCPICA 180  
 QY 175 LIPDENPSSFCNLIIRHIOVSHTLEYPDLOPNIIEPALIRVLDORSLIE 224  
 Db 181 SMWGDIPNRSANPFRHIGRPHRESYDIFVDVDEDMNMCVLQESILD 230

## RESULT 9

US-09-764-864-837  
 ? Sequence 837, Application US/09764864  
 ? Patent No. US20020132753A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Rosen et al.  
 ? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ? FILE REFERENCE: PT223  
 ? CURRENT APPLICATION NUMBER: US/09/764,864  
 ? CURRENT FILING DATE: 2001-01-17  
 ? Prior application data removed - consult PALM or file wrapper  
 ? NUMBER OF SEQ ID NOS: 1792  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 837  
 ? LENGTH: 231  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 ? FEATURE:  
 ? NAME/KEY: SITE  
 ? LOCATION: (16)  
 ? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-864-837

Query Match 27.7%; Score 348; DB 10; Length 231;  
 Host Local Similarity 31.3%; Pred. No. 4, 6e-25;

Matches 72; Conservative 51; Mismatches 85; Indels 22; Gaps 0;  
 QY 8 DSKSAPASATAPALPPRPDPPELVTSFPCVACLEVLHQVPVTCGVHPCRSYIATSLKN 67  
 Db 10 DSKSAPASATAPALPPRPDPPELVTSFPCVACLEVLHQVPVTCGVHPCRSYIATSLKN 62  
 QY 68 NKMTGPGYCAVLEHGVAVTAVAKPKSKYKAWAPPTVTSIMRAHIFGQYLUKY 125  
 Db 63 KRIYGVCPSSALAPGVPAVLEFPGESTETSCHEGPKNFELSKLASHVATQSY 120  
 QY 127 --GPDLELEETAR-----GVPPG--GPELYEYSLDHCITHHSEPPVPCVLCR 174  
 Db 121 MEGVAKATIKDASLOPBNVNPRTFPYFPEKPNQDEGLVECKPLPHSTDTKRSVCPICA 180  
 QY 175 LIPDENPSSFCNLIIRHIOVSHTLEYPDLOPNIIEPALIRVLDORSLIE 224  
 Db 181 SMWGDIPNRSANPFRHIGRPHRESYDIFVDVDEDMNMCVLQESILD 230

## RESULT 10

US-09-998-667-10  
 ? Sequence 10, Application US/09998667  
 ? Patent No. US20020146747A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Masuda, Esteban  
 ? APPLICANT: Zhao, X. Charles  
 ? APPLICANT: Zhu, Peter  
 ? APPLICANT: Pardo, Jorge  
 ? APPLICANT: Pige, Pharmacologists, Incorporated  
 ? TITLE OF INVENTION: TRAC1, Modulators of Lymphocyte Activation  
 ? FILE REFERENCE: 021044-000600US  
 ? CURRENT APPLICATION NUMBER: US/09/998,667  
 ? CURRENT FILING DATE: 2001-12-03  
 ? Prior application data removed - consult PALM or file wrapper  
 ? NUMBER OF SEQ ID NOS: 60/282,432  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 10  
 ? LENGTH: 50  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: human TRAC1  
 US-09-998-667-10

Query Match 23.0%; Score 289; DB 10; Length 50;  
 Host Local Similarity 100.0%; Pred. No. 2, 5e-20;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 VTSFPCVACLEVLHQVTRHGVHPCRSYIATSLKNKMTGPGYCAVLEH 81  
 Db 1 VTSFPCVACLEVLHQVTRHGVHPCRSYIATSLKNKMTGPGYCAVLEH 50

## RESULT 11

US-09-764-864-841  
 ? Sequence 841, Application US/09764864  
 ? Patent No. US20020132753A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Rosen et al.  
 ? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ? FILE REFERENCE: PT223  
 ? CURRENT APPLICATION NUMBER: US/09/764,864  
 ? CURRENT FILING DATE: 2001-01-17  
 ? Prior application data removed - consult PALM or file wrapper  
 ? NUMBER OF SEQ ID NOS: 1792  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 841  
 ? LENGTH: 285  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens



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0Y 5 12SDJCKSAFAASAIADALDKKKRRLPELVTSFDGAGELVYLDQVPTPGCHGVCSCAATS 64
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 LHTDRSASPTPVPPFPGGCKKKPKVKTVEKYECPGCHLIVTSFKOTEGHGFCSMAAL 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 65 LKNNKWTGYCAVPIPSERVATDVAKR-----MKSEYKNCAL----- 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 LSSSSPKTACQSTIKRQVFKINCKCPFLIALDLYCNFNSPGFAEGLMLDLYEKNDC 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y -----DTLVGLSEKMAHILTKCKYTD-----KYLQLELEELAAKVC 141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 HPEELDQVPPDKKRYKLVPLDLKIDHAKAKYKFAALDSQNSGVYMAIALQKHEIDTPPV 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 142 PFCGLYEDSLIDGCTTHRCDE KRPVQVQICE 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VSGTHKQVGYTH PSL SAHT SPQVAAKSTGCPFR 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 6 LKNNKRTCPGCAVATJSECVPAITVAK-----MSEKKNFAE-----1020
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DY 81 LSSSSKRTACQNSYKRVKPKINCKRELLALQYTCNKNESGCAHOLTLGHLVHLKND 1490
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 103 -----CDTLVLTSEMRBAHLRTQOKYID-----KYGPJOLEETFAKCV 1400
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DY 141 CHEEELQCVVPEKKEVLFKNDLREHIVFACTKTFATCSKQVIMIAMQHHDLDCVCV 2000
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 141 CPFCQRELYPDSLLOHCTHHNSE--RRPVCPFLCK 174
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DY 201 VWSQPIKQCVQTLIRSELSAHLSTCVNAASTSEK 236
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Search completed. June 18, 2007, 17:32:12  
Job time : 24 secs

RESULT 15  
 US-08-813-423A-2  
 Sequence 2, Application US/08813323A  
 Patent No. US20020041522A1  
 GENERAL INFORMATION:  
 APPLICANT: Baltimore, David  
 APPLICANT: Cheng, Genhong  
 APPLICANT: Cleary, Aileen  
 APPLICANT: Federman, Seth  
 APPLICANT: Ye, Zheng-sheng  
 TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham, LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/813,423A  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 50659  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ. ID NO.: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 568 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..568  
 US-08-813-423A-2

Query Match	11.78;	Score 147;	DB 8;	Length 568;
Host Local Similarity	22.79;	Pred. No. 1.2e-05;		
Matches 49;	Conservative 26;	Mismatches 95;	Indels 46;	Gaps 4

[illegible]







[illegible]

	Query Match	11.7%	Score 146.57	EB 2	Length 630
	Post Local Similarity	25.4%	Prod. No. 0.00016		
	Matches	622	Conserved	21	Mismatches 537
					Indels 777
					Gaps 12
QY	47	CAWLEFLVHQVWTRGCHVPRKST	ATSLKNKKTKCPYRA	-----	77
Idb	14	CTGCTEPEEPKIPVYCHPDSST	NETWAWGDSFYCTPSYGRARPLAKRIVLCHV	-----	72
QY	78	---YLPSF---GVATIV---	AKPKSPKKN---ASVDTT	WLSMPATIPGCGYITFYCR	128
Idb	73	VDFGFLGADLRKIPATVWTP	PARASAPSNQVACDH---CLKE---AAVKTC-----		119
QY	129	LCHELEIAARCVWTPQREL-----	YEOSLDDHCITTHRSRGRVYV		171
Idb	120	-----LWMASTVQHT	QHPFSPAPQVCHPTQPEVRLPRLPKQSGNNR---LREPTCP		169
QY	172	-----GRLIPDSE---NPSFS	185		
Idb	170	ENSEPCTCHCTVHKTKSPASTS	192		

REFSET: 6  
 1996.2  
 oestrogen responsive finger protein - mouse  
 O:Species: Mus musculus (house mouse)  
 O:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1996  
 C:Accession: 14964.2  
 K:Name: A.; Name: S.; Ikeda, K.; Noji, S.; Muramatsu, M.  
 J: Biol. Chem. 270: 24406-24414, 1995  
 A:Title: Molecular cloning, structure, and expression of mouse estrogen-responsive finger  
 A:Accession: 14964.2; MIM:3925845; PMID:752654  
 A:Protein: 14964.2  
 A:Status: preliminary; translated from cDNA/EST/DBD  
 A:Molecule type: mRNA  
 A:Positions: 1-544 - RRS  
 A:Cross-references: CH:053902; NID:q1088456; PDB:BA07941.1; PDB:q1088467  
 C:Superfamily: RING finger homology  
 C:Keywords: zinc  
 F:9-59/domain: RING finger homology - RING

Query Match	11.5%	Score 144.5	DB Z	Length 634
Host Local Similarity	23.9%	Prod No. 90923		
Matches	562	Conservative	20	Mismatches 57; Indels 83; Gaps 10
QY	37	CAVLEFLVLPYKIRGIVYKRSGLATS--LKNKKKTCPPYR-----		76
Db	13	CSGLLEKPEKPPITTHGHSFSLDLDEWVAGGPPYRPPQYKRYGVYRPLQKNTVMYAV		72
QY	77	--AYLDSKGVPA-----TLVAKRMKSEYKNCACEDTCLVSEMDHRIKQKYLKRYDPL		129
Db	73	VDFGLDAPLARIYVDIMIPPAHFSASSATQVACDH--CLTEIA--VKTC-----		118
QY	130	QLEELFAKVCVCPQVDFEL-----YEDSLDLCITHHSESPPEVC--		171
Db	119	-----LVMANSTVLEHLRPIHFSAPVQHPDLSPIRLDLRRKCIQHNH--LKEPFECE		169
QY	172	YFLLPLTETNSPSTSNLIRHVGCHT		197

ID 17045ECLFQMD.....VFHFVPSPI 186

RESULT 7  
JC7387  
testis-abundant inner protein - human  
C/Spoofed Homo sapiens (man)  
Cloned 17-Nov-2009 #sequence\_finished 17 Nov 2009 #text\_change 06-Feb-2009  
CAccession JC7387  
Reference Acc Yamashita T, Tomimaru N, Yamashita Y, Hishinuma I, Okada K, Suzuki R.  
Biochem Biophys Res Commun 276: 45-51, 2009  
Article Molecular cloning of testis-abundant inner protein, IIRP, from rat liver  
A Reference number JC7387

A:Accession:J07487  
 A.Molecule type: mRNA  
 A.Residues: 1518 (601)  
 A.Cross references: DDBJ:AB044861  
 A.Comment: This protein, a member of the ribonuclease P family, is a protein that is involved in the processing of the 5' end of the 16S rRNA.  
 A.Cepecies: *Escherichia coli*  
 A.Accession: U00096  
 A.Map position: 62013-62014  
 A.Feature: 1518 (601)  
 A.Family: ribonuclease P family  
 A.Function: ribonuclease P activity  
 A.Keywords: collid coll; testis

Query Match 11.4% Score 14.5 E08.2 Length 518  
 Best Local Similarity 25.4% Prob No. in db 45  
 Matches 48; Conservative 40; Mismatches 57; Indels 54; Gaps 9

```

QY      1 RPASTAAALPEEPPEPPELPIVSEAWLTVEIHLGVEFQENHVSQTATSIKNNKW---70
           ||||| ||| : ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB      11 ASAAIAAALNIHQ-----VASASVLETFEIVIEIRGNTPAKT-----TWQW 58
           ||| | | | | | | | | | | | | | | | | | | | | | | | |
QY      71 -----TDPYD-----KAYLSGVVAIIHWAPRNSKN-----C 100
           ||| | | | | | | | | | | | | | | | | | | | | | | |
DB      59 LEEPEPEVETLSPYSPTPLNPGDSMVELAVSLGWPKERLDQSTPGHPAI SLEG 116
           ||| | | | | | | | | | | | | | | | | | | | | | |
QY      101 ACDILWLSERRAHITLCQNYLRKYGLQGLLELAACVGPFGPHLYEISLLHHITTH 160
           ||| | | | | | | | | | | | | | | | | | | | | | |
DB      119 YHGDAVTLTAISHTHDTHTVVLHGAIFRYEELCKRTLELPDQKIQE----- 170
           ||| | | | | | | | | | | | | | | | | | | | | | |
QY      161 HRS--ERRP 167
           ||| | | | |
DB      171 KSSSEKKP 179

RESULT 8
S68467
Clnt: receptor-associated protein CAP-1 human
O.Species: Homo sapiens (man)
C.Date: 17 Jul 1998 #sequence_revision 17 Jul 1998 #text_change 09 Nov 2000
C.Accession: S68467;154498
R.Saito, I.Y. Tite, S.J. Reed, J.C.
FEBS Lett. 358, 113-118, 1995
A.Title: A novel member of the TRAF family of putative signal transducing proteins b
A.Reference number: 154498; M01039512992; PMID:7540216
A.Accession: S68467
A.Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1543 (SAT)
A.Cross-references: EMBL:U48509; NID:q95557; PIRIN:AAA01951.1; FID:q95558
A.Experimental source: tissue-type: total brain
O.Gene(s):
A.Gene: CAP-1
C.Superfamily: Clnt: receptor-associated protein CAP-1; RING finger homology
C.Keywords: homodimer; signal transduction; zinc finger
P:19-97/Domain: RING finger homology - RND
```

Query Match	11.58	Score	142.51	Id#	2	Length	45
Host Local Similarity	24.08	Prod. No.	000027				
Matches	43	Conserved	26	Mismatches	15	Indels	27
							67







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us-09-998-667-1

us-09-998-667-1





```

[4]
LN SEQUENCE FROM N.A.
RX MEDLINE 9507 9981; PubMed 7527023;
PA Hu H.M., O'Kourko K., Bonuski M.S., Dixit V.M.;
KI 7A novel KIM1 ligand protein interacts with the cytoplasmic domain of
KI CD40.
PL J. Biol. Chem. 269:30069-30072(1994).
CC 1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
CC 2- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
CC ASSOCIATED FACTORS (POTENTIAL).
CC 3- SIMILARITY: CONTAINS 1 KIM1-TYPE ZINC FINGER.
CC 4- SIMILARITY: CONTAINS 1 MATH/TRAFF DOMAIN.
CC 5- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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CC or send an email to license@sb.slb.ch).
CC
EMBL: D21092; AAC58112.1;
EMBL: U19260; AAA65732.1;
EMBL: L48509; AAA68195.1;
EMBL: U19647; AAA67531.1;
GENE: BCN112033; TRAF3.
MIM: 601896.
LN INTERPRO: IPR002083; MATH.
LN INTERPRO: IPR003007; TRAF.
LN INTERPRO: IPR001293; Znf_TNFRF.
LN INTERPRO: IPR001841; Znf_C3HC4.
LN Pfam: PF00097; Znf_C3HC4.1.
LN Pfam: PF00917; MATH.1.
LN Pfam: PF02176; Zf_TNFRF.2.
LN SMART: SM00184; KIM1.1.
LN PROSITE: PS00518; ZF_KIM1.1.
LN PROSITE: PS00519; ZF_KIM1.2.
LN PROSITE: PS00519; ZF_TNFRF.2.
KW Zinc-finger; Coiled coil; Repeat.
FT ZN_FING: 68 77 KIM1-TYPE.
FT ZN_FING: 135 190 TRAF-TYPE 1.
FT ZN_FING: 191 249 TRAF-TYPE 2.
FT DOMAIN: 267 338 COILED COIL (POTENTIAL).
FT DOMAIN: 418 503 MATH/TRAFF.
FT CONFLICT: 129 129 I -> M (IN REF. 2 AND 4).
FT CONFLICT: 134 134 MISSING (IN REF. 4).
FT CONFLICT: 218 242 MISSING (IN REF. 3).
FT CONFLICT: 339 339 P -> S (IN REF. 3).
FT CONFLICT: 405 405 K -> Q (IN REF. 4).
SQ SEQUENCE 548 AA; 64460 MW; 6765534B95269B CR664;

Query Match 11.7% Score 147; DB 1; Length 548;
Best local similarity 22.7%; Pred. No. 1; 0-05;
Matches 49; Conservative 26; Mismatches 95; Indels 46; Gaps 4.

```

```

LN 201 VWSYUHRVSV111KSEI SARI SEVWNAUSTRK 246
RESULT 4
LN 2147_HUMAN STANDARD; PRT; 600 AA.
AC Q14258;
ID 15-OCT-2001 (Ref. 40; Unreviewed)
ID 15-OCT-2001 (Ref. 40; Last sequence update)
ID 15-JUN-2002 (Ref. 41; Last annotation update)
ID Zinc finger protein 147 (Estrogen-responsive liver protein) (E1P).
GN ZNF147 or EEP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eulipotyria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
KC TISSUE: placenta.
RX MEDLINE-9408455; PubMed-8248217;
PA Inoue S., Umino A., Hosoi T., Kondo S., Toyoshima H., Kondo T.,
PA Ikegami A., Kohli Y., Umino H., Muramatsu M.;
KI *Genomic binding-site cloning reveals an estrogen-responsive gene that
KI encodes a KIM1 ligand protein.
KI Proc. Natl. Acad. Sci. U.S.A. 90:11117-11121(1993).
LN [2]
LN SEQUENCE FROM N.A.
KC TISSUE: lymph.
KA Submitted (REV 2001) to the EMBL/GenBank/DDBJ databases.
CC 1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
CC 2- SIMILARITY: CONTAINS 1 KIM1-TYPE ZINC FINGER.
CC 3- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
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CC
EMBL: D21205; BAA04747.1;
EMBL: BC016924; AAH16924.1;
GENE: BCN12932; ZNF147.
MIM: 600453;
LN INTERPRO: IPR001879; Gamma_carboxylase.
LN INTERPRO: IPR003878; SPRY_domain.
LN INTERPRO: IPR003877; SPRY_receptor.
LN INTERPRO: IPR001841; Znf_fing.
LN Pfam: PF00622; Zf_C3HC4.1.
LN Pfam: PF00622; SPRY.1.
LN SMART: SM00184; KIM1.1.
LN SMART: SM00449; SPRY.1.
LN PROSITE: PS00518; ZF_KIM1.1.
LN PROSITE: PS00519; ZF_KIM1.2.
LN PROSITE: PS00519; ZF_TNFRF.2.
KW Zinc-finger; Coiled coil.
FT ZN_FING: 13 54 KIM1-TYPE.
FT DOMAIN: 217 407 COILED COIL (POTENTIAL).
FT DOMAIN: 509 600 SPRY.
SQ SEQUENCE 600 AA; 70999 MW; 4E4E21CF0A0000 CR64;

Query Match 11.7% Score 146.5; DB 1; Length 600;
Best local similarity 25.6% Pred. No. 1; 0-05;
Matches 72; Conservative 23; Mismatches 53; Indels 79; Gaps 12;

```

DB 73 VEQFIQADLAKPPADWVTPPARASADSPNAQVACDH -CLKE- AAVKTC----- 119  
 QY 129 LQLEETARCVPCQREL-----YESLLDHCTTHRSERKVP-CP- 171  
 DB 120 -----LVCMASHQCHLPHFDSAPQDHPPLQPPVDILPRKCSQNRK-LREFFCP- 169  
 QY 172 -----LCRLPDE-----NPSFS 185  
 DB 170 HESCEICHCIVKRTCSFASLS 192

## RESULT 5

2147 MOUSE

ID 2147 MOUSE STANDARD: PRT: 634 AA.  
 AC Q61510:

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Zinc finger protein 147 (tripartite motif protein 25) (testogen  
 responsive finger protein) (TFP).  
 GN ZNF147 OR TRIM25 OR ZFP147 OR EFP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090:  
 RN 11

## SEQUENCE FROM N.A.

RP TISSUE-Testis; Ovary; and placenta;  
 RC MEDLINE:96025835; PubMed 7592654;

RA Orino A., Inoue S., Ikeda K., Noji S., Muramatsu M.;  
 RT "Molecular cloning, structure, and expression of mouse estrogen-  
 responsive finger protein 147. Its activation with estrogen receptor  
 RNA in target organs."

RT J. Biol. Chem. 270:24406-24413(1995).  
 CC 1-1 FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.  
 CC 1-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC 1-1 SIMILARITY: CONTAINS 1 SPRY DOMAIN.  
 CC

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CC FMBL: D63902; BAA09441.1;  
 CC MGDI: MG1102749; Trm25.

DR InterPro: IPR001870; Gamma\_carboxylase.  
 DR InterPro: IPR003878; SPRY\_domain.

DR InterPro: IPR003877; SPRY\_receptor.  
 DR InterPro: IPR001841; Znf\_Tfmg.

DR Pfam: PF00097; Zf-C3HC4\_1.  
 DR Pfam: PF03622; SPRY\_1.

DR SMART: SM00184; RING\_1.  
 DR SMART: SM00449; SPRY\_1.

DR PROSITE: PS00518; ZF\_RING\_1.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.

KM Zinc-finger; Coiled coil.  
 FT ZN-FING 13 54 RING-TYPE  
 FT DOMAIN 215 405 COILED COIL (POTENTIAL);  
 FT DOMAIN 514 631 SPRY.

SEQUENCE 634 AA; 71772 MW; 669529DPC83DE611 CRC64;

Query Match 11.5%; Score 144.5; DB 1; Length 634;  
 Best local similarity 23.8%; Prod. No. 26-05;  
 Matches 50; Conservative 20; Mismatches 57; Indels 83; Gaps 10;

QY 47 CAVLELVHVPVRCGVPCQSLATS-LKNNKVCPCGR----- 76  
 DB 13 CAVLELVHVPVRCGVPCQSLATS-LKNNKVCPCGR----- 76  
 QY 77 -AVI PSCVPA-----IIVAKPKSPVKNAPFTVI VTI SPFHAI RFGVYIIVPV 179

DB 73 VEQFIQADLAKPPADWVTPPARASADSPNAQVACDH -CLKEA--VKTC----- 118  
 QY 140 QLEETARCVPCQREL-----YESLLDHCTTHRSERKVP-CP- 171  
 DB 119 -----LVCMASHQCHLPHFDSAPQDHPPLQPPVDILPRKCSQNRK-LREFFCP- 169  
 QY 172 -----LCRLPDE-----NPSFS 185  
 DB 170 HESCEICHCIVKRTCSFASLS 192

## RESULT 6

RN23\_HUMAN

ID RN23\_HUMAN STANDARD: PRT: 518 AA.  
 AC Q96IB6:

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RING finger protein 23 (testis-abundant finger protein) (tripartite  
 motif-containing protein 39).  
 GN TRIM39 OR RNF23 OR TRP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606:  
 RN 11

## SEQUENCE FROM N.A. (ISOFORM 1).

RP TISSUE-Testis;  
 RC MEDLINE:20462913; PubMed 11006080;

RA Orino A., Yamagishi T., Tomioka N., Yamauchi Y., Hishinuma T.,  
 RA Ikeda K., Suzuki M., Sato M., Noji Y., Suzuki H., Inoue S.,  
 RA Yoshimura K., Shimizu Y., Muramatsu M.;  
 RT "Molecular cloning of testis-abundant finger protein/ring finger  
 protein 23 (RNF23), a novel RING-box-coiled coil-B30.2 protein on  
 the class I region of the human MHC."

RT Biochem. Biophys. Res. Commun. 276:45-51(2000).  
 CC 1-1  
 CC

CC SEQUENCE FROM N.A. (ISOFORM 2).  
 CC

RP TISSUE-Colon;  
 RA Strausberg R.;

CC 1-1 ALTERNATIVE PRODUCTS: 2 isoforms; 1 (short form) and 2; may be  
 CC 1-1 TISSUE SPECIFICITY: Ubiquitous; highly expressed in testis.  
 CC 1-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC 1-1 SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.

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CC FMBL: AB046381; BAB16374.1;  
 CC MGDI: BC007661; AAH07661.1;

DR ESTD: P15919; IRM0.  
 DR GENE: HGNC:10065; TRIM39.

DR InterPro: IPR001878; Gamma\_carboxylase.  
 DR InterPro: IPR003878; SPRY\_domain.

DR InterPro: IPR003877; SPRY\_receptor.  
 DR InterPro: IPR003841; Znf\_Tfmg.

DR Pfam: PF00097; Zf-C3HC4\_1.  
 DR Pfam: PF03622; SPRY\_1.

DR Pfam: PF00643; Zf-B-box\_1.  
 DR SMART: SM00336; BBOX\_1.

DR SMART: SM00184; RING\_1.  
 DR SMART: SM00449; SPRY\_1.

[OK	EMUL: AH046382; BARI6375.1; -.
[OK	USSP: P15919; 1RMD.
[OK	MDJ: M61:1890559; R0124.

TO C<sub>60</sub> AND THE LYMPHOTOXIN ACTA RECEPTOR (BY SIMILARITY)  
-1 SUBUNIT: HOMOPOLYMER OR HETEROLOGIC WITH OTHER IN-PROTEIN-  
-1 ASSOCIATED FACTORS (POTENTIAL)

```

CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN, ALSO FOUND IN
CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY, NOT
CC FOUND IN LIVER.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5 HIGHEST
CC LEVELS FOUND BETWEEN E11.5 AND E14.5, AT LATE STAGES OF GESTATION,
CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
CC -1- SIMILARITY: CONTAINS 1 ZINC-FINGER ZINC FINGER
CC -1- SIMILARITY: CONTAINS 1 ZINC-FINGER ZINC FINGER
CC -1- SIMILARITY: CONTAINS 2 ZINC-FINGER ZINC FINGER.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: 021050; AAC52175.1;
CC EMBL: 038440; AAC52710.1;
CC MGI: MGI:108041; Trf13.
CC InterPro: IPRO02083; MATH
CC InterPro: IPRO01007; TRAF
CC InterPro: IPRO01293; Znf_TRAF
CC InterPro: IPRO01841; Znf_TRAF
CC Pfam: PF00947; Zf-CRHC4; 1.
CC Pfam: PF00947; MATH; 1.
CC Pfam: PF02176; Zf-TRAF; 2.
CC SMART: SM00061; MATH; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00516; ZF_RING_1; 1.
CC PROSITE: PS00516; ZF_RING_2; 1.
CC PROSITE: PS01451; ZF-TRAF; 2.
CC ZINC-FINGER: Coiled coil; Repeat.
CC ZN_FING 67 76 PING-TYPE.
CC ZN_FING 134 189 TRAF-TYPE 1.
CC ZN_FING 190 248 TRAF-TYPE 2.
CC DOMAIN 266 337 COILED COIL (POTENTIAL).
CC DOMAIN 417 502 MATH/TRAF.
CC CONFLICT 72 73 CF -> WO (IN REF. 2).
CC CONFLICT 490 490 T -> M (IN REF. 2).
CC SEQUENCE 567 AA; 6425 MW; 2522B3484119DC CRC64;

```

Query Match: 11.74, Score: 142, E-Value: 567,  
 Best Local Similarity: 24.28; Field No: 2,96 CG;  
 Matches: 45; Conservative: 22; Mismatches: 73; Indels: 46; Gaps: 4;

```

CC 45 FPCAVCLEVHDPRTGCHVFCRSIATSLKNNKMTCPYCAVLDSGVPAIVAKP 92
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 50 YKPKKPVVGNPKPTGTGHPFSCMAALLSSSKKTKNCGESIKRKVEFDNCKRPI 109
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 93 -----MRSYKNCAR 129
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 110 LADVGVCRNDRGCAEDLTGHLVHLKNNQPEELLCALPKCKEVLAKKLDPEVERAG 169
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 121 KLVV-----KRVGDELEIAAPVYPCGCHLELDESLLEHLEHSE--PRVY 193
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 170 KYRATCSHCKSOVPMKIKKHEDTGVVWVSCPRGCVGLLRELSAHLSEVNAVS 229
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC
CC 169 FCPURK 174
CC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CC 230 TCSFKR 235

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RESULT 9  
 RAG1\_HUMAN STANDARD: PRT; 1043 AA.  
 AC P15918;  
 DT 01-APR-1990 (Ref. 14, Created)  
 DT 01-APR-1990 (Ref. 14, Last sequence update)  
 DT 15-JUN-2002 (Ref. 41, Last annotation update)  
 DE V(D)J recombination activating protein 1 (Rag-1).  
 GN RAG1.

```

CC Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NC_004106.6;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE-94329570; PubMed-8052643;
CC Schatz D G., Cellinger M A., Baltimore D.;
CC "The V(D)J recombination activating gene, RAG-1."
CC Cell 59:1035-1048(1989).
CC [2]
CC IDENTIFICATION OF IMPORTIN ALPHA 1 BINDING DOMAIN.
CC MEDLINE-94329570; PubMed-8052643;
CC Cortes P., Ye Z.-S., Baltimore D.;
CC "RAG-1 interacts with the repeated amino acid motif of the human
CC homolog of the yeast protein SRP1."
CC Proc. Natl. Acad. Sci. U S A 91:7643-7647(1994).
CC [3]
CC VARIANT: CYS 244 AND HIS 249.
CC MEDLINE-97061229; PubMed-8644221;
CC Nandodon J.F., Lase A., Seminato R., Rubiol E., Haiget M., Soler J.;
CC "Two new variants of RAG-1 protein predicted by SSCP."
CC Hum. Mutat. 8:191-192(1996).
CC [4]
CC VARIANTS SCID HIS-624 AND LYS-722, AND VARIANT VAL-156.
CC MEDLINE-96412253; PubMed-8810255;
CC Schwartz K., Cause G.H., Lodwig L., Panigro U., Li Z., Linde D.,
CC Friedrich W., Seger R.A., Hansen-Hagge T.E., Desiderio S.,
CC Lieber M.R., Bartman C.R.;
CC "RAG mutations in human B cell-negative SCID."
CC Science 274:97-99(1996).
CC [5]
CC VARIANTS OS C 396, H 396, C-429, H 561, C 561, H 747 AND C-912.
CC MEDLINE-98292185; PubMed-9530231;
CC Villa A., Santagata S., Bozzi F., Gillani S., Fratini A., Imberti L.,
CC Gatta L.B., Occhi H.D., Schwarz K., Notarangelo L.P., Vezzoni P.,
CC Spanopoulou E.;
CC "Partial V(D)J recombination activity leads to omenn syndrome."
CC Cell 93:885-896(1998).
CC [6]
CC VARIANTS OS C-196 AND APO-887.
CC MEDLINE-20074845; PubMed-10606976;
CC Wada T., Takai K., Kudo M., Shimura S., Kasahara Y., Koizumi S.,
CC Kase H., Ishida Y., Imashiro S., Seki H., Yoshie A.;
CC "Characterization of immune function and analysis of RAG gene
CC mutations in Omenn syndrome and related disorders."
CC Clin. Exp. Immunol. 119:148-155(2000).
CC [7]
CC 1. PUNCTION: DURING LYMPHOCYTE DEVELOPMENT, THE GENES ENCODING
CC IMMUNOGLOBULINS AND T CELL RECEPTORS ARE ASSEMBLED FROM VARIABLE
CC (V), DIVERSITY (D), AND JOINING (J) GENE SEGMENTS. THIS
CC COMBINATORIAL PROCESS, KNOWN AS V(D)J RECOMBINATION, ALLOWS THE
CC GENERATION OF AN ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A
CC LIMITED AMOUNT OF GENETIC INFORMATION. THE RAG1/RAG2 COMPLEX
CC INITIATES THIS PROCESS BY BINDING TO THE CONSERVED RECOMBINATION
CC SIGNAL SEQUENCES (RSS) AND INTRODUCING A DOUBLE-STRAND BREAK
CC BETWEEN THE RSS AND THE ADJACENT CODING SEQUENCE. THESE BREAKS ARE
CC FOLLOWED BY TWO STEPS, NICKING OF ONE STRAND (HYPERMUTATION),
CC PROMOTED BY HAIRPIN FORMATION (TRANSDUCTION). RAG1/2 HAS
CC ALSO BEEN SHOWN TO FUNCTION AS A TRANSPOSASE IN VITRO, AND TO
CC PROMOTE RSS-INDEPENDENT ENDONUCLEASE ACTIVITY (END PROCESSING) AND
CC HAIRPIN OPENING. RAG1 ALONE CAN BIND TO RSS BUT STABLE, EFFICIENT
CC BINDING REQUIRES RAG2. ALL KNOWN CATALYTIC ACTIVITIES REQUIRE THE
CC PRESENCE OF BOTH PROTEINS.
CC -1- COFACTOR: Binds 1 megadalton or megadalton for per substrate (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: MATURING LYMPHOID CELLS.
CC -1- DOMAIN: THE SPECIFIC BINDING TO THE NONAMER RSS MOTIF IS MEDIATED
CC BY THE NONAMER BINDING DOMAIN (NBD).
CC -1- DISEASE: DEFECTS IN RAG1 ARE A CAUSE OF SEVERE COMBINED
CC IMMUNODEFICIENCY, B CELL-NEGATIVE (B-) SCID.
CC -1- DISEASE: DEFECTS IN RAG1 ARE A CAUSE OF OMENN SYNDROME (OS); A
CC SEVERE IMMUNODEFICIENCY CHARACTERIZED BY THE PRESENCE OF

```



```

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC      frameshift in position 419.
CC -----
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CC -----
DR EMBL: J03776; AAA0073.1; ALT_FRAME.
DR EMBL: AF220014; AAG53468.1; -.
DR EMBL: AF220015; AAG53469.1; -.
DR EMBL: AF220016; AAG53470.1; ALT_INIT.
DR EMBL: BC005447; AAH05447.1; -.
DR PIR: A30891; A30891.
DR HSSP: P28940; 1CHC.
DR MDL: MG198178; Trf10.
DR InterPro: IPR001870; Gamma_carboxyl.
DR InterPro: IPR003878; SPRY_domain.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR00315; Znf_Box.
DR InterPro: IPR01841; Znf_Tfnq.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF03422; SPRY; 1.
DR Pfam: PF03443; zf_Box; 1.
DR PRINTS: PR01406; BROXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Transcription regulation; DNA-binding; Trans-acting factor;
KW Zinc-finger; Nuclear protein; Alternative splicing.
KW ZNF_RING; 15 59
FT FT_78_FING 91 132 E_BOX_TYPE.
FT FT_79_FING 347 495 SPRY.
FT FT_80_FING 205 210 HIGHLY HYDROPHILIC.
FT FT_81_FING 268 276 NEGATIVE REGULATION SIGNAL (POTENTIAL).
FT FT_82_FING 145 151 CALKIRM -> SHHHEL (IN ISOP-DM BETA).
FT FT_83_FING 152 156 MISSING (IN ISOP-DM BETA).
FT FT_84_FING 68 68 E -> K (IN REF. 4).
FT FT_85_FING 148 148 W -> R (IN REF. 4).
FT FT_86_FING 241 241 E -> Q (IN REF. 4).
FT FT_87_FING 268 268 T -> S (IN REF. 4).
FT FT_88_FING 416 416 K -> N (IN REF. 4).
FT FT_89_FING 437 437 R -> C (IN REF. 4).
FT FT_90_FING 437 437 R -> C (IN REF. 4).
FT FT_91_FING 437 437 R -> C (IN REF. 4).
FT FT_92_FING 437 437 R -> C (IN REF. 4).
FT FT_93_FING 437 437 R -> C (IN REF. 4).
FT FT_94_FING 437 437 R -> C (IN REF. 4).
FT FT_95_FING 437 437 R -> C (IN REF. 4).
FT FT_96_FING 437 437 R -> C (IN REF. 4).
FT FT_97_FING 437 437 R -> C (IN REF. 4).
FT FT_98_FING 437 437 R -> C (IN REF. 4).
FT FT_99_FING 437 437 R -> C (IN REF. 4).
FT FT_100_FING 437 437 R -> C (IN REF. 4).
FT FT_101_FING 437 437 R -> C (IN REF. 4).
FT FT_102_FING 437 437 R -> C (IN REF. 4).
FT FT_103_FING 437 437 R -> C (IN REF. 4).
FT FT_104_FING 437 437 R -> C (IN REF. 4).
FT FT_105_FING 437 437 R -> C (IN REF. 4).
FT FT_106_FING 437 437 R -> C (IN REF. 4).
FT FT_107_FING 437 437 R -> C (IN REF. 4).
FT FT_108_FING 437 437 R -> C (IN REF. 4).
FT FT_109_FING 437 437 R -> C (IN REF. 4).
FT FT_110_FING 437 437 R -> C (IN REF. 4).
FT FT_111_FING 437 437 R -> C (IN REF. 4).
FT FT_112_FING 437 437 R -> C (IN REF. 4).
FT FT_113_FING 437 437 R -> C (IN REF. 4).
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FT FT_115_FING 437 437 R -> C (IN REF. 4).
FT FT_116_FING 437 437 R -> C (IN REF. 4).
FT FT_117_FING 437 437 R -> C (IN REF. 4).
FT FT_118_FING 437 437 R -> C (IN REF. 4).
FT FT_119_FING 437 437 R -> C (IN REF. 4).
FT FT_120_FING 437 437 R -> C (IN REF. 4).
FT FT_121_FING 437 437 R -> C (IN REF. 4).
FT FT_122_FING 437 437 R -> C (IN REF. 4).
FT FT_123_FING 437 437 R -> C (IN REF. 4).
FT FT_124_FING 437 437 R -> C (IN REF. 4).
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FT FT_127_FING 437 437 R -> C (IN REF. 4).
FT FT_128_FING 437 437 R -> C (IN REF. 4).
FT FT_129_FING 437 437 R -> C (IN REF. 4).
FT FT_130_FING 437 437 R -> C (IN REF. 4).
FT FT_131_FING 437 437 R -> C (IN REF. 4).
FT FT_132_FING 437 437 R -> C (IN REF. 4).
FT FT_133_FING 437 437 R -> C (IN REF. 4).
FT FT_134_FING 437 437 R -> C (IN REF. 4).
FT FT_135_FING 437 437 R -> C (IN REF. 4).
FT FT_136_FING 437 437 R -> C (IN REF. 4).
FT FT_137_FING 437 437 R -> C (IN REF. 4).
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FT FT_139_FING 437 437 R -> C (IN REF. 4).
FT FT_140_FING 437 437 R -> C (IN REF. 4).
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FT FT_143_FING 437 437 R -> C (IN REF. 4).
FT FT_144_FING 437 437 R -> C (IN REF. 4).
FT FT_145_FING 437 437 R -> C (IN REF. 4).
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FT FT_147_FING 437 437 R -> C (IN REF. 4).
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FT FT_151_FING 437 437 R -> C (IN REF. 4).
FT FT_152_FING 437 437 R -> C (IN REF. 4).
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FT FT_154_FING 437 437 R -> C (IN REF. 4).
FT FT_155_FING 437 437 R -> C (IN REF. 4).
FT FT_156_FING 437 437 R -> C (IN REF. 4).
FT FT_157_FING 437 437 R -> C (IN REF. 4).
FT FT_158_FING 437 437 R -> C (IN REF. 4).
FT FT_159_FING 437 437 R -> C (IN REF. 4).
FT FT_160_FING 437 437 R -> C (IN REF. 4).
FT FT_161_FING 437 437 R -> C (IN REF. 4).
FT FT_162_FING 437 437 R -> C (IN REF. 4).
FT FT_163_FING 437 437 R -> C (IN REF. 4).
FT FT_164_FING 437 437 R -> C (IN REF. 4).
FT FT_165_FING 437 437 R -> C (IN REF. 4).
FT FT_166_FING 437 437 R -> C (IN REF. 4).
FT FT_167_FING 437 437 R -> C (IN REF. 4).
FT FT_168_FING 437 437 R -> C (IN REF. 4).
FT FT_169_FING 437 437 R -> C (IN REF. 4).
FT FT_170_FING 437 437 R -> C (IN REF. 4).
FT FT_171_FING 437 437 R -> C (IN REF. 4).
FT FT_172_FING 437 437 R -> C (IN REF. 4).
FT FT_173_FING 437 437 R -> C (IN REF. 4).
FT FT_174_FING 437 437 R -> C (IN REF. 4).
FT FT_175_FING 437 437 R -> C (IN REF. 4).
FT FT_176_FING 437 437 R -> C (IN REF. 4).
FT FT_177_FING 437 437 R -> C (IN REF. 4).
FT FT_178_FING 437 437 R -> C (IN REF. 4).
FT FT_179_FING 437 437 R -> C (IN REF. 4).
FT FT_180_FING 437 437 R -> C (IN REF. 4).
FT FT_181_FING 437 437 R -> C (IN REF. 4).
FT FT_182_FING 437 437 R -> C (IN REF. 4).
FT FT_183_FING 437 437 R -> C (IN REF. 4).
FT FT_184_FING 437 437 R -> C (IN REF. 4).
FT FT_185_FING 437 437 R -> C (IN REF. 4).
FT FT_186_FING 437 437 R -> C (IN REF. 4).
FT FT_187_FING 437 437 R -> C (IN REF. 4).
FT FT_188_FING 437 437 R -> C (IN REF. 4).
FT FT_189_FING 437 437 R -> C (IN REF. 4).
FT FT_190_FING 437 437 R -> C (IN REF. 4).

```



[illegible]



## SIMILARITY: CONTAINS 1 SPRY DOMAIN.

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EMBL: 009425; AAA9431.1;  
 EMBL: AF00517; BAB6330.1;  
 Genbank: H3NF.12962; IRIM26;  
 MIM: 600830;  
 UniProt: IPK01870; Gamma-carboxyiso;  
 UniProt: IPK01878; SPRY\_domain;  
 UniProt: IPK01877; SPRY\_receptor;  
 UniProt: IPK00115; Znf\_Box;  
 UniProt: IPK01841; Znf\_Box;  
 P100: P00097; Zf-CR4; 1;  
 P100: P00622; SPRY; 1;  
 P100: P00643; Zf-B\_Box; 1;  
 PRINTS: PR01406; BBOXZNFINTER;  
 SMART: SM0036; BBOX; 1;  
 SMART: SM0084; RING; 1;  
 SMART: SM0049; SPRY; 1;  
 PROSITE: PS0119; ZF-BBOX; 1;  
 PROSITE: PS00518; ZF-RING\_1; FALSE\_NRG;  
 PROSITE: PS0089; ZF-RING\_2; 1;  
 K0 Zinc-finger; Collod coil;  
 F1 ZN\_RING 16 57 RING-TYPE;  
 F1 ZN\_RING 97 138 B\_BOX-TYPE;  
 F1 DOMAIN 188 227 COILED COIL (POTENTIAL);  
 F1 DOMAIN 465 539 SPRY;  
 F1 DOMAIN 488 400 POLY-GLO;  
 F1 DOMAIN 422 432 POLY-GLO;  
 SEQUENCE: 649 AA: 62165 MM: 842A71G1FE2348 GC664;

Query Match: 10.0%; Score 126; 108 1; Length 539;

Best Local Similarity: 26.7%; Prod. NO: 0.00072;

Matches 41; Conservative 40; Mismatches 58; Indels 44; Gaps 9;

07 16 SATAKATERRRPPETPVTSPTAVCI FVLHPPVTPGSHVCPSCG--ATSLKNNKWTCP 74  
 11 1111 11 11111111 11 11111111 11 11111111 11 11111111  
 08 4 SAPLRSLER-----VF--GSLGLYLRPPVITLGGHVFCKSCITDVPITSGSKVCP 54  
 07 74 YKAVTDSNV-PATVA-----KPKK-SFYNNFAP-111VLSMPAHITQVRY10K 125  
 11  
 08 55 LCKKFKKKNIRPWAJLAVFNIRPKVKGQPSG-----VTEQQAQKLEGRER 108  
 07 126 YGHLGELLETAGKVCPCQK-----ELYEDSLDRCITFHR 162  
 11  
 08 109 ---LHYVTDGKILAVYMCRRSRHRHIVAMKKAQVIREKTNLSTLR 158

Search completed: June 18, 2003, 17:27:51

Job time : 25 secs

1  
2  
3  
4

5  
6

GenScore version 5.1.6  
Copyright (c) 1994 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: June 18, 2003, 17:27:22 ; Search time 80 Seconds

(without alignments)  
597,537 Million cell updates/sec

Lib file: US-09-998-667-1

Sequences: 1 MOSVUSUSKSAFASAAAR.....LIKRVLSKSLIYVNSNII 212

Scoring table: B1/S0M62 Gapop 10.0 ; Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum lib seq length: 0

Maximum lib seq length: 200000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMHL\_21:  
1: SP\_archaea:  
2: SP\_bacteria:  
3: SP\_fungi:  
4: SP\_humans:  
5: SP\_invertebrates:  
6: SP\_mammals:  
7: SP\_mhc:  
8: SP\_ornathio:  
9: SP\_phage:  
10: SP\_plant:  
11: SP\_robot:  
12: SP\_virus:  
13: SP\_vertebrates:  
14: SP\_unclassified:  
15: SP\_virus:  
16: SP\_bacteriophage:  
17: SP\_archaeal:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHMAB1P5

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	100.0	232	4	Q9NXX39
2	1224	97.4	232	4	Q9EBD8
3	1197	95.2	232	6	Q9E8F1
4	1004	79.8	288	11	Q9C3H2
5	726	57.8	163	11	Q9D9R0
6	336	26.7	237	4	Q9A437
7	303	24.1	248	11	Q9D9M9
8	293	23.5	245	11	Q9C3F6
9	287	22.8	245	4	Q9BWD3
10	273	22.2	245	4	Q9B16
11	224.5	17.9	178	11	Q9C3A4
12	213	17.0	209	11	Q9FBD2
13	209	16.6	209	11	Q9ATB9
14	191	15.2	128	4	Q9D0M0
15	182.5	14.5	184	4	Q9D8B7
16	165	13.1	151	4	Q9B8K2

17	160.5	12.8	475	5	Q9D0A4	Q9D0A4 diosaphila
18	160.5	12.8	475	5	Q9B319	Q9B319 diosaphila
19	156.5	12.5	530	11	Q9D196	Q9D196 mus musculus
20	155.5	12.4	557	4	Q9D464	Q9D464 homo sapien
21	155	12.3	522	4	Q9Y4K4	Q9Y4K4 homo sapien
22	152.5	12.1	626	11	Q9Z2R9	Q9Z2R9 mus musculus
23	149.5	11.9	463	5	Q9XG99	Q9XG99 diosaphila
24	148.5	11.8	558	11	Q9L140	Q9L140 mus musculus
25	148.5	11.8	558	11	Q9L191	Q9L191 mus musculus
26	143.5	11.4	516	4	Q9D447	Q9D447 homo sapien
27	142.5	11.3	528	13	Q9L885	Q9L885 xenopus lae
28	141	11.2	428	5	Q9YJ95	Q9YJ95 diosaphila
29	141	11.2	451	5	Q9B8F3	Q9B8F3 diosaphila
30	139.5	11.1	504	3	Q9B626	Q9B626 sc hirose ch
31	137.5	10.9	406	3	Q9D0F0	Q9D0F0 sc hirose ch
32	136.5	10.9	468	3	Q9P308	Q9P308 sc hirose ch
33	136	10.8	426	11	Q9Q882	Q9Q882 mus musculus
34	135	10.8	445	11	Q9Q884	Q9Q884 mus musculus
35	133.5	10.6	1047	6	Q9K463	Q9K463 mus musculus
36	133	10.6	413	11	Q9B8K0	Q9B8K0 mus musculus
37	133	10.6	417	4	Q9Y598	Q9Y598 homo sapien
38	133	10.6	417	11	Q9D568	Q9D568 mus musculus
39	133	10.6	417	11	Q9B8S2	Q9B8S2 mus musculus
40	132.5	10.5	961	13	Q9B8A8	Q9B8A8 talus gall
41	131.5	10.5	599	5	Q9E8X5	Q9E8X5 diosaphila
42	131.5	10.5	1079	13	Q9D0E1	Q9D0E1 phorobites
43	131	10.4	95	11	Q9B1S0	Q9B1S0 mus musculus
44	130.5	10.4	1098	4	Q9D8D7	Q9D8D7 homo sapien
45	130	10.3	425	10	Q9K744	Q9K744 arabid-fusis

#### ALIGNMENTS

RESULT 1  
Q9NXX39 PRELIMINARY PRI: 232 AA.  
DI 01-OCT-2000 (TREMHL01: 15, created)  
DI 01-OCT-2000 (TREMHL01: 15, last sequence update)  
DI 01-JUN-2002 (TREMHL01: 21, last annotation update)  
DE CINA FLJ20456 (15, clone KAI09827.  
US Homo sapiens (Human).  
US Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
NX NBI\_Ltaxid:9606;  
KN [1]  
KF SEQUENCE FROM N.A.  
KA Watanabe K., Yamada A., Takaya S., Yamaguchi M., Tashiro H., et al.  
KA Sasaki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,  
KA Nakamura Y., Isonai T., Saito S.,  
KI "Nippon human cDNA sequencing project".  
KT Saito T. (1999) "The FMD database".  
NC -1- SIMILARITY CONTAINS 1 KING TYPE ZINC FINGER.  
DE EMBL: AK004643; BAA91182.1;  
DE HSSP: P15919; IRM0.  
DE InterPro: IP000562; FN Type-11.  
DE InterPro: IP001841; Z1 Type-11.  
DE Pfam: PF00067; Z1-C00041; 1.  
DE SMART: SM00059; FN2: 1.  
DE SMART: SM00184; FN2: 1.  
DE PROSITE: PS00418; ZF FN1\_1; 1.  
KW Zinc-finger.  
SQ  
SEQUENCE: 232 AA: 23481 MG: IATGQFATAC217AA Q9NXX39.

Query Match 100.0% Score 1257.7 db 4: length 232  
Post local similarity 100.0% Prod. No. 3 db 1:1  
Matches 232: conservative of: Mus musculus of: Indels of: gaps of:

QY 1 MOSVUSUSKSAFASAAAR.....LIKRVLSKSLIYVNSNII Q9NXX39 60  
II 1 MOSVUSUSKSAFASAAAR.....LIKRVLSKSLIYVNSNII Q9NXX39 60  
II 1 MOSVUSUSKSAFASAAAR.....LIKRVLSKSLIYVNSNII Q9NXX39 60

```

UY 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
DB 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
UY 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
DB 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
UY 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 232
    |||
DB 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 232
    |||

```

## RESULT 2

```

O96EOR ID O96EOR PRELIMINARY: PRT: 232 AA.

```

```

AC O96EOR:
DB 01-DEC-2001 (TREMblrel, 19, created)
DB 01-DEC-2001 (TREMblrel, 19, last sequence update)
DB 01-JUN-2002 (TREMblrel, 21, last annotation update)
DB Unknown (protein for MG021737).
DB Homo sapiens (Human).
DB Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
DB Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
DB NCBI_TaxID=9606;
DB RN
DB SEQUENCE FROM N.A.
DB TISSUE-TESTIS, AND EMBRYONAL (ACACINOMA;
DB Strausberg R.;
DB Submitted (JUN-2001) to the EMBL/Genbank/Trna databases
DB EMBL: BC012021; AAI12021; 1;
DB InterPro: IPR000822; 201_C2H2;
DB InterPro: IPR001841; 201_Fing;
DB Pfam: PF00097; 21_C2H2C4; 1;
DB SMART: SM00355; 20F_C2H2; 2;
DB PROSITE: PS00518; 2F_RING_1; UNKNOWN_1;
DB RNA binding; Zinc-finger;
DB KW
DB SEQUENCE 232 AA; 26496 MW; 7358DBA190C79877 CRC64;

```

Query Match 97.4%; Score 1224; PR 4; Length 232.

Best Local Similarity 97.8%; Pred. No. 7.8e-118;

Matches 226; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

```

UY 1 MMSVLSSTSGKSAVASAPALPPPPDPPIVTSPPAVAVI PVI HQVPTGCHVPCRS 60
    |||
DB 1 MMSVLSSTSGKSAVASAPALPPPPDPPIVTSPPAVAVI PVI HQVPTGCHVPCRS 60
    |||
UY 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
DB 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
UY 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
DB 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
UY 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 231
    |||
DB 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 231
    |||

```

```

O95KFI ID O95KFI PRELIMINARY: PRT: 232 AA.

```

```

AC O95KFI:
DB 01-DEC-2001 (TREMblrel, 19, created)
DB 01-DEC-2001 (TREMblrel, 19, last sequence update)
DB 01-JUN-2002 (TREMblrel, 21, last annotation update)
DB Hypothetical 26.2 kDa protein.
DB Mammalia: Craniata: Vertebrata: Euteleostomi:
DB Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
DB Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:
DB Cercopithecoidea: Macaca

```

```

UY NCBI_TaxID 9541;
DB NCBI_TaxID 9541;
UY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
UY TISSUE-TEMPORAL LOBE RIGHT;
DB TISSUE-TEMPORAL LOBE RIGHT;
UY Suzuki Y., Hida M., Kusuda T., Taniguchi K., Iizumi M., Terao K.,
DB Suzuki Y., Hida M., Kusuda T., Taniguchi K., Iizumi M., Terao K.,
UY Isolation of full-length cDNA clones from macaque brain cDNA
DB Isolation of full-length cDNA clones from macaque brain cDNA
UY libraries.
DB libraries.
UY Submitted (APR-2001) to the EMBL/Genbank/Trna databases.
DB Submitted (APR-2001) to the EMBL/Genbank/Trna databases.
UY EMBL: A0060918; BAB46910.1;
DB EMBL: A0060918; BAB46910.1;
UY InterPro: IPR000822; 201_C2H2;
DB InterPro: IPR000822; 201_C2H2;
UY InterPro: IPR001841; 201_Fing;
DB InterPro: IPR001841; 201_Fing;
UY Pfam: PF00097; 21_C2H2C4; 1;
DB Pfam: PF00097; 21_C2H2C4; 1;
UY SMART: SM00355; 20F_C2H2; 2;
DB SMART: SM00355; 20F_C2H2; 2;
UY PROSITE: PS00518; 2F_RING_1; UNKNOWN_1;
DB PROSITE: PS00518; 2F_RING_1; UNKNOWN_1;
UY RNA binding; Zinc-finger;
DB RNA binding; Zinc-finger;
UY KW
DB KW
UY SEQUENCE 232 AA; 26204 MW; 07134D21084D0D7F CRC64;

```

Query Match 95.2%; Score 1197; PR 6; Length 232.

Best Local Similarity 95.7%; Pred. No. 4.6e-115;

Matches 222; Conservative 2; Mismatches 8; Indels 0; Gaps 0.

```

UY 1 MMSVLSSTSGKSAVASAPALPPPPDPPIVTSPPAVAVI PVI HQVPTGCHVPCRS 60
    |||
DB 1 MMSVLSSTSGKSAVASAPALPPPPDPPIVTSPPAVAVI PVI HQVPTGCHVPCRS 60
    |||
UY 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
DB 61 IATSLKNNKWTGPGVAVLPSPGVAVPAAVAKPMKSEYKCAECGDTVLTSEMPAHITPCG 120
    |||
UY 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
DB 121 KYIDKYGPGPLPFTAAAPVCPGCPGPELVESLIDHCITHHKSRPPVPCVPLIDEN 180
    |||
UY 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 232
    |||
DB 181 PSSFSNGLIRHLOVSHITLYDFIDFNIEFALLIRKVLKSLLEYVNSHT 232
    |||

```

## RESULT 4

```

O95CH2 ID O95CH2 PRELIMINARY: PRT: 288 AA.

```

```

AC O95CH2:
DB 01-JUN-2001 (TREMblrel, 17, created)
DB 01-JUN-2001 (TREMblrel, 17, last sequence update)
DB 01-JUN-2002 (TREMblrel, 21, last annotation update)
DB 493053F04RIK protein (Fragment).
DB 493053F04RIK protein (Fragment).
UY Mus musculus (Mouse).
DB Mus musculus (Mouse).
UY Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
DB Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
UY Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.
DB Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.
UY NCBI_TaxID=10090;
DB NCBI_TaxID=10090;
UY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
UY STRAIN=C57BL/6J; TISSUE=TESTIS;
DB STRAIN=C57BL/6J; TISSUE=TESTIS;
UY MIMLNIP:21085660; PubMed:11217851;
DB MIMLNIP:21085660; PubMed:11217851;
UY Kawat J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
DB Kawat J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
UY Aikawa T., Hara A., Eukunishi Y., Kono H., Adachi T., Fukuoka S.,
DB Aikawa T., Hara A., Eukunishi Y., Kono H., Adachi T., Fukuoka S.,
UY Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
DB Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
UY Saito T., Okazaki Y., Gojohori T., Bono H., Kusaka T., Saito R.,
DB Saito T., Okazaki Y., Gojohori T., Bono H., Kusaka T., Saito R.,
UY Kadota K., Matsuda H.A., Ashburner M., Batada S., Casavant T.,
DB Kadota K., Matsuda H.A., Ashburner M., Batada S., Casavant T.,
UY Eletschmann W., Gaasterland T., Gissi C., King R., Korchwa H.,
DB Eletschmann W., Gaasterland T., Gissi C., King R., Korchwa H.,
UY Kuehl P., Lewis S., Matsuda Y., Nikaudo I., Presotto G., Quackenbush J.,
DB Kuehl P., Lewis S., Matsuda Y., Nikaudo I., Presotto G., Quackenbush J.,
UY Schmitt L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio T.,
DB Schmitt L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio T.,
UY Sakai K., Okada T., Furuno M., Aono H., Baidarrelli P., Barsh G.,
DB Sakai K., Okada T., Furuno M., Aono H., Baidarrelli P., Barsh G.,
UY Blake J., Ballell D., Bojunga N., Carninci P., de Bonaldo M.F.,
DB Blake J., Ballell D., Bojunga N., Carninci P., de Bonaldo M.F.,
UY Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
DB Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
UY Gashinich S., Hill D., Hofmann M., Howe D.A., Kanaya M., Lee N.H.,
DB Gashinich S., Hill D., Hofmann M., Howe D.A., Kanaya M., Lee N.H.,
UY Gyros P., Marchionni L., Mashima J., Mazzarelli J., Mombertis P.,
DB Gyros P., Marchionni L., Mashima J., Mazzarelli J., Mombertis P.,
UY Reiche F., Ring B., Ritschard M., Rotherbach T., Sakamoto N.,
DB Reiche F., Ring B., Ritschard M., Rotherbach T., Sakamoto N.,
UY Sasaki H., Sato K., Schenck G., Soga T., Shibata Y., Storch K.-F.,
DB Sasaki H., Sato K., Schenck G., Soga T., Shibata Y., Storch K.-F.,
UY Suzuki H., Toyooka K., Wang K.H., Wenz G., Whitaker C., Wilming L.,
DB Suzuki H., Toyooka K., Wang K.H., Wenz G., Whitaker C., Wilming L.,

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QY 158 ITHRESPPEPPTGCTTCFNNSSSTGNIHDEVSHTLTYCTETLLEFALLPEV 237  
 DB 170 VESHRSDPNKVPVPTCSAMPWQWPKSKANLQHLHHRKSYDTFVPSIDEEAAGAA 229

QY 218 LORSLLE 224  
 DB 230 LAUSTRSE 236

## RESULT 7

QY099M9 PRELIMINARY: PRT: 248 AA.  
 ID QY099M9  
 DT 01-JUN-2001 (TREMURel. 17, Created)  
 DT 01-JUN-2001 (TREMURel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMURel. 20, Last annotation update)  
 DE 1700045119RIK protein.  
 GN 1700045119RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NBI\_TaxID=10090;

SEQUENCE FROM N.A.  
 KC SIKAIN-c57hu/64; TISSUE=TESTIS;  
 KC MEDLINE=21095660; PubMed=11217851;  
 KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 KA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 KA Akawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 KA Saito T., Okazaki Y., Gotohori T., Bito H., Kasukawa T., Saito K.,  
 KA Fletchman W., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 KA Fletchman W., Gasterland T., Gissi G., King H., Kochwa H.,  
 KA Kuchl I., Lewis S., Matsuo Y., Nikaido T., Hosole G., Otakebush J.,  
 KA Schmitt I., Staudt F., Suzuki F., Tomita M., Wagner L., Washio T.,  
 KA Sakai K., Oshida T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 KA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 KA Brownstein M.J., Bull C., Fletcher C., Fujita K., Gariboldi M.,  
 KA Gustriuch S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,  
 KA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
 KA Nordone P., Pflug B., Pflanz M., Rodiguez C., Sakamoto N.,  
 KA Sasaki H., Sato K., Schoenbach G., Soya T., Shibata Y., Storch K.F.,  
 KA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker G., Wilming L.,  
 KA Wyszynski-Boris A., Yoshida K., Yasogawa Y., Kawaji H., Kohsaki S.,  
 KA Hayashizaki Y.,  
 KA "Functional annotation of a full-length mouse cDNA collection."  
 KL Nature 409:685-690(2001).  
 CC EMBL: AK010486; BAB26977.1;  
 CC FMBL: AK006700; BAB24708.1;  
 DR MGI:1921514; 1700045119RIK.  
 DR InterPro: IPR000822; ZNF\_C2H2.  
 DR InterPro: IPR001841; ZNF\_C104.  
 DR Pfam: PF000947; ZF-C10C4.1.  
 DR SMART: SM00184; FING. 2.  
 DR SMART: SM00355; ZNF\_C2H2.1.  
 KW Zinc Finger.  
 SQ SQUONCE: 248 AA; 28399 MW; 96297A194C65466 CPG64.

Query Match 24.18; Score 303; DB 11; Length 248;

Best Local Similarity 40.94; Prod. No. 4.20 23;

Matches 72; Conservative 29; Mismatches 90; Indels 42; Gaps 6;

QY 35 FDCAVGLVLIHOPVTRGCGHVGRCSCATSLKNNKWTGPRATVSP---GVPAADV 89  
 DB 17 FVCPGVGEVKTIVPAACKRVKCKCHLSAKKESHLGCPICRGVTRERACVRAVDL 76  
 QY 90 AKRMSEYKCAVDITLVLSKPAHILPTCKYTIKYG----- 127  
 DB 77 FTIMRHPCNGCRGCGKQVRLHYMKQHYKCEKYGPFRVSTVSSEFGQSPNSVNSNEA 136  
 QY 128 -----ELQLEETAA K-VCPGRVRL-ELYEDSLDQHTTHRSRRRVEVPLAK 174  
 DB 137 PASANAEVLQEEFENASPPDEFTFDKPLCEFTVMSKORLIDHGNSSHGKRAVAVICPTCL 196

QY 175 LLEGEHNSSTGNIHDEVSHTLTYCTETLLEFALLPEV 227  
 DB 197 SLPWGDPPTTFNEVSHLNQRPFRGAPVNLGQTFQVQALTESF--HVN 247

## RESULT 8

QY099M9 PRELIMINARY: PRT: 245 AA.  
 ID QY099M9  
 DT 01-JUN-2001 (TREMURel. 17, Created)  
 DT 01-JUN-2001 (TREMURel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMURel. 20, Last annotation update)  
 DE 2410015A17RIK protein.  
 GN TP1F 09 2410015A17RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NBI\_TaxID=10090;

SEQUENCE FROM N.A.  
 KC SIKAIN-c57hu/64; TISSUE=EMBRYONIC STEM CELLS, AND EMBRYO;  
 KC MEDLINE=21095660; PubMed=11217851;  
 KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 KA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 KA Akawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 KA Saito T., Okazaki Y., Gotohori T., Bito H., Kasukawa T., Saito K.,  
 KA Fletchman W., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 KA Fletchman W., Gasterland T., Gissi G., King H., Kochwa H.,  
 KA Kuchl I., Lewis S., Matsuo Y., Nikaido T., Hosole G., Otakebush J.,  
 KA Schmitt I., Staudt F., Suzuki F., Tomita M., Wagner L., Washio T.,  
 KA Sakai K., Oshida T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 KA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 KA Brownstein M.J., Bull C., Fletcher C., Fujita K., Gariboldi M.,  
 KA Gustriuch S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,  
 KA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
 KA Nordone P., Pflug B., Pflanz M., Rodiguez C., Sakamoto N.,  
 KA Sasaki H., Sato K., Schoenbach G., Soya T., Shibata Y., Storch K.F.,  
 KA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker G., Wilming L.,  
 KA Wyszynski-Boris A., Yoshida K., Yasogawa Y., Kawaji H., Kohsaki S.,  
 KA Hayashizaki Y.,  
 KA "Functional annotation of a full-length mouse cDNA collection."  
 KL Nature 409:685-690(2001).  
 CC EMBL: AK010486; BAB26977.1;  
 CC FMBL: AK006700; BAB24708.1;  
 DR MGI:1922211; Trif.  
 DR InterPro: IPR000822; ZNF\_C2H2.  
 DR InterPro: IPR001841; ZNF\_C104.  
 DR Pfam: PF000947; ZF-C10C4.1.  
 DR SMART: SM00184; FING. 2.  
 DR SMART: SM00355; ZNF\_C2H2.1.  
 KW Zinc Finger.  
 SQ SQUONCE: 245 AA; 28399 MW; 96297A194C65466 CPG64.

Query Match 23.58; Score 295; DB 11; Length 245;

Best Local Similarity 28.74; Prod. No. 4.80 23;

Matches 69; Conservative 35; Mismatches 84; Indels 44; Gaps 6;

QY 25 FVZAVLTLVLIHOPVTRGCGHVGRCSCATSLKNNKWTGPRATVSP---GVPAADV 89  
 DB 16 FVCPGVGEVKTIVPAACKRVKCKCHLSAKKESHLGCPICRGVTRERACVRAVDL 76  
 QY 87 IIVAKMSEYKCAVDITLVLSKPAHILPTCKYTIKYG-----PLQLEETAAAC 139  
 DB 76 ENIMREFSG---SCWQSKRIKRYMKQHYKCEKYGPFRVSTVSSEFGQSPNSVNSNEA 142  
 QY 140 -----VCEQORELY-ESLIDHGTTHRSRRRVEVPLAK 174  
 DB 133 PSTETASINTEVYGGTSSSHPTPKVYQPSNPTKGLITDGNSSHTEGQVAVTPTIC 192  
 QY 174 KILPDENSSPSCGNIHDEVSHTLTYCTETLLEFALLPEV 227  
 DB 193 SLPWGDPPTTFNEVSHLNQRPFRGAPVNLGQTFQVQALTESF--HVN 247

## RESULT 9

QWV03

UNWV03 PRELIMINARY: PRI: 245 AA.

AT QWV03:

DT 01 MAR 2002 (TREMUR01, 20, created)

DT 01 MAR 2002 (TREMUR01, 20, last sequence update)

DT 01 JUN 2002 (TREMUR01, 21, last annotation update)

DT Hypothetical 28.2 KDa protein.

OS Homo sapiens (Human).

CA Eukaryota; Eubacteria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eubacteria; Primates; Catarrhini; Hominoidea; Homo.

NX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE (ERO3);

RA Submitted 8.2

RE Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

LR EMBL: W078107; AHH107.1; .

LR InterPro: IPR001841; Z01\_1191

LR Pfam: PF00037; Z1-C3HC4; 1.

LR SMART: SM00184; RING; 2.

LR ProSITE: PS0089; ZF\_RING\_2; 1.

LR Hypothetical protein.

NX SEQUENCE: 245 AA; 28192 MW; 80784500809196 GC64;

UNWV Match 22.88; Score 287; DB 4; Length 245;

Host Local Similarity 29.88; Prod. No. 1.8e-21;

Matches 67; Conservative 41; Mismatches 89; Indels 48; Gaps 6;

QY 45 EWAVTEVLEHQPVR-TROGVEKRSATSLKNNKWTGYVAVLP SEVE AHV R9

DB 15 FYGVGVGVKLEPRITAVGVHVPKPKRTTAMKSSAPPPGPGVNIPEPKA-PEPAALD 95

QY 90 AKPKKSPYKNAAPYVTVVLSMPAHLPYQKYLKQY----- 127

DB 76 ENIMKKSQSTPQAKQIKFYPMHMYKSKKYQGVGVSSILPNPQISQSVGNNSRSE 145

QY 128 -----PIQELFEIARGV--GPRGREL--EGLSLDHGTHHSEKRYVGPRLK 176

DB 136 TSTDNLEIYQENISSSHHTFKPKIQESNTPKPIHQNSNHLQIVVIVGVSIL 195

QY 177 PDEKSSPSNIPHLGVSHITPYDEPTENITFEALPPVDPSS 221

DB 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240

QY 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240

QY 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240

QY 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240

QY 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240

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QY 196 PWUPQSUTTNFVSHLMGRKQFVGVGVNIQIIPPTGYGVAVRPS 240





Job time : 82 secs

FA Takahashi S., Fujii A., Oshima A., Shioyama A., Kikawaki H.,  
 Nakagawa S., Nishihara T., Masuda Y., Nagai K., Igarashi T.,  
 FU "Mammalian cDNA sequencing project."  
 FU Submitting (v1.2001) to the EMBL/GenBank/TrEMBL databases.  
 FU EMBL: AK057201; BABY1480.1; --  
 FU Init.c:Pro: 118002950; Jost\_2PH2.  
 FU Init.c:Pro: 118000422; Jost\_2PH2.  
 FU P1am: PF02809; 01M: 1.  
 FU SMART: SMO0455; ZNF\_02H2; 2.  
 FU PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 1.  
 FU DNA: 110104; Zinc finger.  
 SU SC000106; 126 AA; 14378 MW; 570A6ED1AAB719640 CRO64;

Query Match	15.2%;	Score 191;	DB 4;	length 128;
Best local Similarity	31.4%;	Pred. No. 6,8e-12;		
Matches	43;	Conservative	17;	Mismatches 43;
				Indels 34;
				Gaps 34;

07 112 MRAHIRFQKYITIKYGPLOGLFEFAAG-----VCPFC-QRE 147  
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 16 1 MRVHLSTCLK-----VCEGMANPKFVPVPPTSLPIPSNIPNRSTFACPCYGARN 50  
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07 148 14910811007TTHHRSERPPVPEICGLPLENLSFSPNLIJHLOVSHLETFMFDPN 207
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10 51 100JELVAKHVSHTGDPNRVVOVTSAMWJUDYSKANNELOHLLHREKFSYDLEVDYS 110

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Q7	208 IFEALIRVLORSILE	224
E6	111 : 1 11 1	
	111 IDEFAATQNALISLE	127

RESULT 15  
Q901P87

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Ac  090F87;
Dt  01-MAY-2000 (TREMblrel, 13, Created)
Dl  01-MAY-2000 (TREMblrel, 13, Last sequence update)

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16 Hypothetical 21.3 kDa protein (Fragment).  
68 DKFZ34411714.  
75 Homo sapiens (Human).

NC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
KN	[1]

RECEIVED TESTIS;  
FA Koether K., Meyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
RE Submitted (DEC-1999) to the EMBL/GenBank/EBI databases.

106 **TestProt**: IP(0.00822; Z(0.0242;  
108 **SMART**: SM0055; Z(0.0242; 1;  
110 **HypotTestProt**: 0.0010.

SU: 21304 MW: E66A58423102128 CR:664  
 Quantity Match: 14.5% Score: 182.5% BH 4: Length: 1837

Matches	46	Conservative	26	Mismatches	67	Indels	33	Gaps	3
86	ATTAAKAAKSEVENAATGTTTATGSEMPAATCTGKYLKYG-								127

10 ADULENIMKESINSPOTAKU IKRYEMKHYSOKKYDUEYVSSITPNEU1SQUVONS 69

128 .....PQIETEARVU-PCUGRELY-ENSLDMCTHHSERKIVYPL 172

174 CRL1PDENDPshSGL1PHLQVSHLLEFYD10HNIIEALIKRVLTKS 271

ED 140 CVALFWOJUSQIIFNFVSHLNGKHQFDYGRFVNIQLDEELGYQIAVERS 178

Search completed: June 18, 2003, 17:40:35

100

100

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